

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:08:07 ; Search time 2527.69 seconds  
(without alignments)  
10174.698 Million cell updates/sec

Title: US-09-770-916-1  
Perfect score: 1588  
Sequence: 1 ccattctcttctcatagc.....taaaaaaaaaaaaaaaaaaa 1588

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estlin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	948	59.7	1576	11	AK007918 Mus muscu
2	830.8	52.3	842	12	BG071858 H3103H12-
3	636.6	40.1	977	10	BE367725 601217516
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ALIGNMENTS

RESULT 1	AK007918	1576 bp	linear	HFC 19-JAN-2002
LOCUS	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length			
DEFINITION	enriched library, clone:181006009:immunoglobulin heavy chain 1 (serum IgG2a), full insert sequence.			
ACCESSION	AK007918	GI:12841780		
VERSION	AK007918.1			
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (strain:C57BL/6J) 10 day old male pancreas cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library clone:181006009.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE 1	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)			
REFERENCE 2	20499374			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			





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BE367725  
BE367725.1 GI:9313153  
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house mouse.  
Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 977)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov  
Tissue procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1AM8748 row: o column: 04  
High quality sequence stop: 735.  
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Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"  
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Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"  
BASE COUNT 275 a 288 c 226 g 188 t  
ORIGIN



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DEFINITION mRNA sequence.
ACCESSION BF136899
VERSION   BF136899.1 GI:10975939
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Tissue Procurement: Gilbert Smith, Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: NCI-CGAP clone distribution information can be
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              Investigator providing samples: Gilbert Smith, NIH"
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Y      564  TCAGTGAAGTGTGAACTCTGGATCCCTGCTGCCAGAGTGTGCACACCTTCCAGCT 623
Y      121  TCAGTGAAGTGTGAACTCTGGATCCCTGCTGCCAGAGTGTGCACACCTTCCAGCT 180
Y      624  CTCTGAGTCTGGAGTCTACACTATGAGGAGTCACTGACTGTCCTCCCTCCAGCACCTGG 683
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DEFINITION mRNA sequence.
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VERSION   BF135247.1 GI:10974287
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
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AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Gilbert Smith, Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: NCI-CGAP clone distribution information can be
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          http://image.llnl.gov
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MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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Query Match      39.2%; Score 621.8; DB 12; Length 754;
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Matches 715; Conservative 0; Mismatches 27; Indels 7; Gaps 7;

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RESULT 6
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OCUS
DEFINITION
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IMAGE:1531775 3', similar to gb:X67210 M.musculus rearranged
immunoglobulin gamma 2b heavy (MOUSE);, mRNA sequence.

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ACCESSION      BE134114
VERSION        BE134114.1
KEYWORDS       GI:8596614
SOURCE         house mouse.
ORGANISM       Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 647)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccgaps@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:947875
High quality sequence stop: 440.
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/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      125 a 140 c 171 g 211 t
ORIGIN

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Query Match      38.1%; Score 604.8; DB 10; Length 647;
Best Local Similarity 97.3%; Pred. No. 3e-115;
Matches 615; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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QY 1068 AGTGGCAAGAGTTCAAAATGCAAGGTCAACACAAAGAGCTCCCATCCATCCGAGAGAG 1127
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QY 1128 ACCATCTCAAAATTAAGGGCTTAGTCAGAGCTCCCAAGTATACATCTTGGCCGCCACCA 1187
Db 452 ACCATCTCAAAATTAAGGGCTTAGTCAGAGCTCCCAAGTATACATCTTGGCCGCCACCA 393
QY 1188 GCAGAGCAGTTGTCCAGGAAAGATGTCACTTCACTTGTGCTGGGTTCACACCT 1247
Db 392 GCAGAGCAGTTGTCCAGGAAAGATGTCACTTCACTTGTGCTGGGTTCACACCT 333
QY 1248 GGAGACATCAGTTGTGAGTGGACCAATGGGCATACAGAGAGAACTACAGAGACACC 1307
Db 332 GGAGACATCAGTTGTGAGTGGACCAATGGGCATACAGAGAGAACTACAGAGACACC 273
QY 1308 GCACAGTCTTGAGTCTGACGGTTCTTACTTATATAGCAAGCTCAATATGAAACA 1367
Db 272 GCACAGTCTTGAGTCTGACGGTTCTTACTTATATAGCAAGCTCAATATGAAACA 213
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 152 TACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAATGAGCTCAGCACCACCAAGC 93  
 1488 TCTCAGGTCTTAAGAGACACTGGCACCCTATCATCCATGCTCCCTTGTATATAAAGCAT 1547  
 92 TTTTCAAGTCTTAAGAGACACTGGCACCCTATCATCCATGCTCCCTTGTATATAAAGCAT 33  
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RESULT 7  
 BF148722/c  
 LOCUS  
 DEFINITION  
 uy34a01.x1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:3661416 3',  
 similar to SW:GCB\_MOUSE P01866 IG GAMMA-2B CHAIN C REGION. ;, mRNA  
 sequence.

ACCESSION  
 VERSION  
 SOURCE  
 KEYWORDS  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 639)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Other ESTs: uy34a01.y1  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Cloning Strategy: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 image.llnl.gov/image/html/iresources.shtml

MG1:1422184  
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 High quality sequence stop: 423.  
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 Site:2: SalI; transgenic model WNT-1, expression driven by  
 MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
 dt. Library constructed by Life Technologies.  
 Investigator providing samples: Gilbert Smith, NIH"  
 122 a 140 c 171 g 205 t 1 others

BASE COUNT 122 a 140 c 171 g 205 t 1 others

ORIGIN

Query Match 37.1%; Score 589; DB 12; Length 639;  
 Best Local Similarity 95.9%; Pred. No. 5,7e-112;  
 Matches 604; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Y 945 CAGATCAGCTGGTTGTGAACACGCTGGAGAGTACACACAGCTCAGACACAAACCATAGA 1004  
 b 630 CAGATCAAGTGGTTGTGAACACGCTGGAGAGTACACACAGCTCAGACACAAACCATAGA 571  
 Y 1005 GAGGATTACACAGTACTATCCCGGTGGTTCAGCACCCTCCCATCCAGCACCAGGACTGG 1064

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 1065 ATGAGTGGCAGAGGTTCAAAATGCAAGGTCAAAACAAAGACCTCCCATCAGCCCATCGAG 1124  
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 210 ACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAAGCTGAGACACGAGGCTCTGAAA 151  
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 150 AATTACTACTCTGAGAGACCATCTCCGGTCTCCGGGTAATGAGCTCAGCACCACAAA 91  
 1485 AGCTCTCAGTCTTAAGAGACACTGGCACCCTATCCATGCTCCCTTGTATATAAATAAG 1544  
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 30 CATCCAGCAAGCCTGGTACCATGTA 1

AA882246 703 bp mRNA linear EST 26-MAR-1998  
 vx42e07.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone  
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 (HUMAN); gb:X67210 M.musculus rearranged immunoglobulin gamma 2b  
 heavy (MOUSE);, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 703)  
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Gessel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenger,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theisinger,B., Wylie,T., Lennop,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 The WashU-HHMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of MedicineP  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MG1:669692  
 Putative full length read  
 vector to vector length is 811



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578 TTGGAATCTCTGGATCCCTGCTCAGCAGTGTGCACACCTTCCAGCTCTCCCTGAGTCG 637  
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310 CGGCCCATTTCAACAATCAACCCCTGCTCCATGCAAGGAGTGTCAACAATGCCAGC 369  
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938 AGAGCTCCAGATCAGCTGGTGTGTGAACAAGCTGGAAGTACACACAGCTCAGACACAAAC 997  
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DEFINITION  
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BM243266.1 GI:17878536  
house mouse.  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 552)  
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,  
Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.  
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell  
(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)  
Unpublished (2001)  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: K0644 row: A column: 12  
Seq primer: -21M13 Forward  
High quality sequence stop: 552  
POLYA=Yes.  
Location/Qualifiers  
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/tissue\_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)"  
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/lab\_host="DH10B"  
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Matches 547; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      103 a 123 c 149 g 172 t
ORIGIN
Query Match      33.8%; Score 536; DB 12; Length 547;
Best Local Similarity 99.1%; Pred. No. 5.6e-101;
Matches 539; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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547 ATCCGGGTGGTCAGTCCCTCCCATCCAGCACAGGACTGGATGGGCAAGGAGTTC 488
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427 AAAGGGCTAGTCAGAGCTCCACAGTATACATCTTGCGCCACACAGAGAGAGTGTGCC 368
1203 AGAAAGATGTGAGTCTGCTGCTGCTGGTGTCAAGGCTTCAACCTGGAGAGATCAGTGTG 1262
367 AGAAAGATGTGAGTCTGCTGCTGCTGGTGTCAACCTGGAGAGATCAGTGTG 308
1263 GAGTGGACCAAGCAATGGGCATACAGAGAGAGAACTACAAGGACACCGCACCTGCTGGAC 1322
307 GAGTGGACCAAGCAATGGGCATACAGAGAGAGAACTACAAGGACACCGCACCTGCTGGAC 248
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7 ACCA 4
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BF134589
BF134589.1 GI:10973629
EST.
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SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 530)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabps@remail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9240 row: f column: 01
High quality sequence stop: 528.
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Location/Qualifiers
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Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      149 a 150 c 126 g 105 t
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Best Local Similarity 99.6%; Pred. No. 4.5e-99;
Matches 528; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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187 ACAGATTCCTTCTCATGCAAGCTGAGACAGAGGCTGTGAAAAATTACTACCTGAAGAAG 128
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127 ACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACCAAGCTCTCAGGTCTTAAGA 68
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7 ACCA 4
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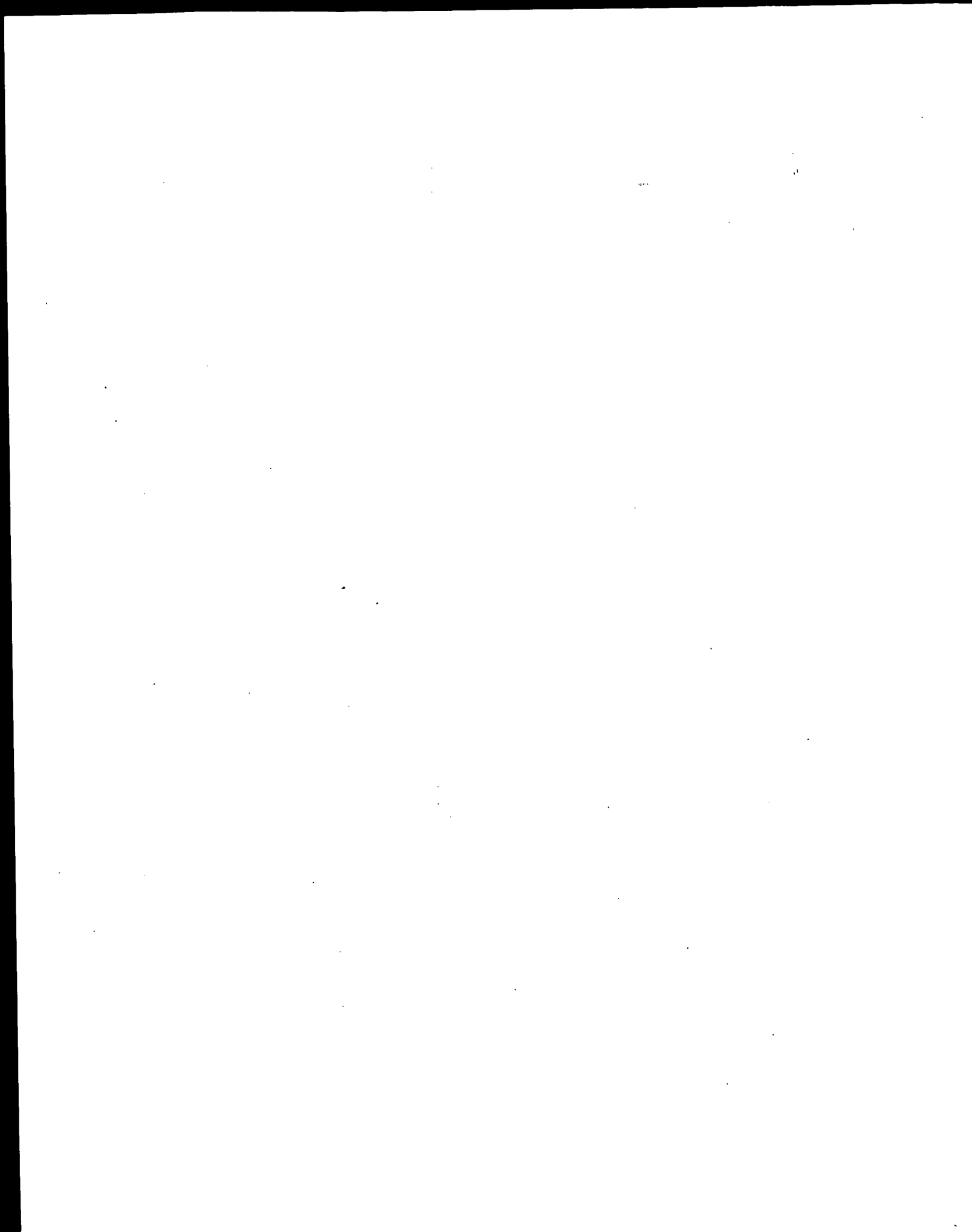




Site\_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt<sup>18</sup>. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH

[illegible]

Search completed: June 24, 2003, 01:19:55  
Job time : 2537.69 secs



result No.	Score	Query		DB	ID	Description
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2	795	50.1	1407	10	US-10-429-662-9	Sequence 9, Appli
3	795	50.1	1407	10	US-10-429-660-9	Sequence 9, Appli
4	781.2	49.2	1407	1	PCT-US02-02373-14	Sequence 14, Appl
5	774	48.7	1109	9	US-10-272-899A-81	Sequence 81, Appl
6	769.2	48.4	1109	9	US-10-272-899A-79	Sequence 79, Appl
7	768.6	48.4	1027	9	US-10-272-899A-21	Sequence 21, Appl
8	763.8	48.1	1027	9	US-10-272-899A-23	Sequence 23, Appl
9	670.6	42.2	1386	1	PCT-US02-3440A-21	Sequence 21, Appl
10	670.6	42.2	1386	1	PCT-US02-35330A-21	Sequence 21, Appl
11	670.6	42.2	1386	9	US-10-286-132A-21	Sequence 21, Appl
12	670.6	42.2	1386	9	US-10-281-479A-21	Sequence 21, Appl
13	670.6	42.2	1398	10	US-10-275-180A-21	Sequence 21, Appl
14	648.8	40.9	1392	10	US-10-384-933-8	Sequence 8, Appli
15	643.6	40.5	1673	9	US-10-342-887-1932	Sequence 1932, Ap
16	643.6	40.5	1673	12	PCT-60-446-133-237	Sequence 237, App
17	639	40.2	1410	1	US-10-292-088-53	Sequence 53, Appl
18	639	40.2	1410	10	US-10-292-088-53	Sequence 53, Appl
19	638.6	40.2	1430	5	US-09-848-832-1	Sequence 1, Appli
20	638.6	40.2	1430	10	US-10-225-108A-1	Sequence 1, Appli





SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 1407

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Humanized

OTHER INFORMATION: CSE10 Heavy Chain Sequence

-T-US02-02373-14

Query Match 49.2%; Score 781.2; DB 1; Length 1407;  
Best Local Similarity 73.3%; Pred. No. 1.6e-194;  
Matches 1056; Conservative 0; Mismatches 348; Indels 36; Gaps 3;

33 ATGGCTGCTTGGGCTGCTCTCTGCTGCTGGTGACATCCCAAGCTGTGCTCTATCCCGAG 92  
|||||  
1 ATGGCTGCTTGAAGCTACTCTCTGCTGGTGAACATTCCTCAAGCTGTATCTTTCCCGAG 60  
93 GTGAGCTGAAGCAGTCAAGGCTGAGCTAGTGCAGCCCTCAGAGGCTGTGCCATCCAC 152  
|||||  
61 GTGAGCTGAAGGAGTCAAGGCTGAGCTGCTGGGCTGCTGAGGCTGTGCCATCCAC 120  
153 TGCACAGCTCTGCTGCTTCTCAATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCT 212  
|||||  
121 TGCACGCTCTCAGGCTTCTCAATTAAGGCTATGCTGCTGCTGCTGCTGCTGCTGCT 180  
213 GGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272  
181 GGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
273 GCTTTCATATCAGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332  
|||||  
241 GCTTTCATATCAGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
333 ATGACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392  
|||||  
301 ATGACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348  
393 ATTTACTATGATTTTCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 452  
|||||  
349 TGTATTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408  
453 TGTATTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512  
|||||  
409 TGTATTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468  
513 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572  
469 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528  
573 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632  
529 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588  
633 ---TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689  
589 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648  
690 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749  
649 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708  
750 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809  
709 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 747  
810 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869  
748 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807  
870 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929  
808 GACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867

QY 930 GATGACCCAGAGCTCCAGATCAGCTGGTTTGTGAACAACGCTGGAAGTACACACAGCTCAG 989  
DB 868 GAAAGACCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 927  
QY 990 ACACAACCCATAGAGAGGATTACACACAGTACTATCCGGTGTGCTCAGCAGCTCCGCCATC 1049  
DB 928 ACAAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 987  
QY 1050 CAGCAGGAGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1109  
DB 988 CAGCAGGAGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1047  
QY 1110 CCATCAGGAGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1169  
DB 1048 CAGCAGGAGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1107  
QY 1170 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1229  
DB 1108 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1167  
QY 1230 GTCGCTGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1289  
DB 1168 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1227  
QY 1290 GAGAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1349  
DB 1228 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1287  
QY 1350 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1409  
DB 1288 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1347  
QY 1410 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1469  
DB 1348 TACATCTTCCGCTGATGATGGCAAGGAGTTCAAATGCAAGGTCACAAACAAACAAACAACTC 1407

## RESULT 5

US-10-272-899A-81  
; Sequence 81, Application US/10272899A  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa L.  
; APPLICANT: Healy, Judith Jacques  
; APPLICANT: Newman, Walter  
; APPLICANT: Ponath, Paul  
; APPLICANT: Bruce Key  
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES, METHODS OF PRODUCTION, AND METHODS OF  
; TITLE OF INVENTION: USE THEREFOR  
; FILE REFERENCE: MP101-244P2RM  
; CURRENT APPLICATION NUMBER: US/10/272,899A  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81  
; LENGTH: 1109  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin cassette sequence Leader-Mu\_WT\_60  
US-10-272-899A-81

Query Match 48.7%; Score 774; DB 9; Length 1109;  
Best Local Similarity 85.1%; Pred. No. 1.2e-192;  
Matches 877; Conservative 0; Mismatches 150; Indels 3; Gaps 1;  
QY 443 AGTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 502  
|||||



77 AGTCACAGTACAGTACGACCAACAAACAGCCCATCGGTCTATCCACTGGGCCCTCTGTGTG 136  
503 TGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCTGTGTCAGAGGCTACTTCCCTGA 562  
137 TGGAGTACAACTGGCTCTCCGTGACTCTAGGATGCTGTGTCAGAGGCTATTTCCCTGA 196  
563 GTCACTGACTGTGACTTGGAACTCTGGATCCCTGTCAGAGTGTGACACACTTCCAGC 622  
197 GCCAGTACCTTGTGACTTGGAACTCTGGTCCCTGTCAGAGTGTGACACACTTCCAGC 256  
623 TCTCTGAGTGTGACTTGTGACTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 682  
257 TCTCTGAGTGTGACTTGTGACTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 316  
683 GCCAAGTACAGACCTGACCTGACGCTGTCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 742  
317 GCCCAGCAGACCTGACCTGACATGTGGCCACCCCGCAGCAGCAGCAGCAGCAGCAGCAGC 376  
743 AAAAATTGAGCCAGCGGCGCCATTTCAACAATCAACCCCTGCTCCATCAAGAGGTG 802  
377 GAAAATTGAGCCAGAGTGCCTAT---AACACAGAACCCCTGCTCCCTCAAGAGGTG 433  
803 TCACAAATGCCAGCTCCTTACCTCGAGGCTGACCATCCGCTCTTCTATCTTCCCTCCAAA 862  
434 TCCCCATGCGCAGCTCCAGACCTTGGGTGGACCATCCGCTCTTCTATCTTCCCTCCAAA 493  
863 TATCAAGGATGTACTCATGATCTCCCTGACACCAAGTCAAGTGTGCTGGTGGTGTG 922  
494 GATCAAGGATGTACTCATGATCTCCCTGAGCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 553  
923 GAGCAGGATGACCCAGCAGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 982  
554 GAGCAGGATGACCCAGCAGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613  
983 AGCTCAGACAAACCCATAGAGAGGATTACAAAGTGTGCTGGTGGTGGTGGTGGTGGTGGT 1042  
614 AGCTCAGACAAACCCATAGAGAGGATTACAAAGTGTGCTGGTGGTGGTGGTGGTGGTGGT 673  
1043 CCCCATCCAGCAGCAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1102  
674 CCCCATCCAGCAGCAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733  
1103 AGACCTCCCATCCATCCAGAGAACCATCTCAAAAATTAAGGGCTAGTCTCAGAGCTCC 1162  
734 AGCCCTCCCATCCCATCCAGAGAACCATCTCAAAAATTAAGGGCTAGTCTCAGAGCTCC 793  
1163 ACAAGTATACATCTTGGCCGACCCAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1222  
794 ACAGGTATATGCTTGTGCTTCCACAGCAGAGAGATGACTTAAGAAAGTGTGCTGCTGCTG 853  
1223 TTGCTGCTGCTGCTGCTTCAACCTTGAGACATCAGTGTGGAGTGGACCAAGTGGGCA 1282  
854 CTGCATGATCACAGGCTTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913  
1283 TACAGAGGAGAACTACAGAGACACCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1342  
914 TACAGAGGAGAACTACAGAGACACCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973  
1343 ATATAGCAAGCTCAATATGAAACAGCAAGTGGGAGAAACAGATTCCTTCTCATGCAA 1402  
974 GTACAGCAAGCTCAGAGTACAAAGAGCACTTGGGAAAGAGGAGTCTTTTTCGCTGCTC 1033  
1403 CGTGAGCAGCAGGCTGTGAAATTAATCTACCTGAAGAACCACTCTCCCGGCTCCCGG 1462  
1034 AGTGGTCCAGAGGCTGTGCAATCACTTACAGCTTAAGACCATCTCCCGGCTCTCGG 1093  
1463 TAAATGAGCT 1472  
1094 TAAATATCT 1103

RESULT 6  
S-10-272-899A-79

; Sequence 79, Application US/10272899A  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa L.  
; APPLICANT: Healy, Judith Jacques  
; APPLICANT: Newman, Walter  
; APPLICANT: Ponath, Paul  
; APPLICANT: Bruce Key  
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,  
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF  
; TITLE OF INVENTION: USE THEREFOR  
; FILE REFERENCE: MP101-244P2RM  
; CURRENT APPLICATION NUMBER: US/10/272,899A  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79  
; LENGTH: 1109  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunoglobulin cassette sequence  
; OTHER INFORMATION: Leader-Mu\_FCR11\_61  
US-10-272-899A-79

Query Match 48.4%; Score 769.2; DB 9; Length 1109;  
Best Local Similarity 84.9%; Pred. No. 2,1e-191;  
Matches 874; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 443 AGTCACGCTCTCTCAGCCAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTG 502  
Db 77 AGTCACAGTACAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 136  
QY 503 TGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCTGTGTCAGAGGCTACTTCCCTGA 562  
Db 137 TGGAGATACAACTGGTTCCTCCGTGACTCTAGGATGCTGTGTCAGAGGCTACTTCCCTGA 196  
QY 563 GTCACTGACTGTGACTTGGAACTCTGGAATCCTGTCAGAGCTGTGTCAGAGCTTCCAGC 622  
Db 197 GCCAGTACCTGACTGGAATCCTGTCCTGTCAGAGCTGTGTCAGAGCTTCCAGC 256  
QY 623 TCTCTGAGTGTGACTTGTGACTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 682  
Db 257 TCTCTGAGTGTGACTTGTGACTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 316  
QY 683 GCCAAGTACAGACCTGACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 742  
Db 317 GCCCAGCAGACCTGACCTGCAATGTGGCCACCCCGCAGCAGCAGCAGCAGCAGCAGCAGC 376  
QY 743 AAAAATTGAGCCAGCGGCGCCATTTCAACAATCAACCCCTGCTCCATCAAGAGGTG 802  
Db 377 GAAAATTGAGCCAGAGTGCCTAT---AACACAGAACCCCTGCTCCCTCAAGAGGTG 433  
QY 803 TCACAAATGCCAGCTCCTTACCTCGAGGCTGACCATCCGCTCTTCTATCTTCCCTCCAAA 862  
Db 434 TCCCCATGCGCAGCTCCAGACCTGCGAGGCTGACCATCCGCTCTTCTATCTTCCCTCCAAA 493  
QY 863 TATCAAGGATGTACTCATGATCTCCCTGACACCAAGTGTGCTGCTGCTGCTGCTGCTGCTG 922  
Db 494 GATCAAGGATGTACTCATGATCTCCCTGAGCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 553  
QY 923 GAGCAGGATGACCCAGCAGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 982  
Db 554 GAGCAGGATGACCCAGCAGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613  
QY 983 AGCTCAGACAAACCCATAGAGAGGATTACAAAGTGTGCTGGTGGTGGTGGTGGTGGTGGT 1042  
Db 614 AGCTCAGACAAACCCATAGAGAGGATTACAAAGTGTGCTGGTGGTGGTGGTGGTGGTGGT 673  
QY 1043 CCCCATCCAGCAGCAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1102





143 TCAGTACGATGTAATGCTTCTGGGTTTCGCGAGACTCCGGAGAGAGGCTGGAGTGGGTGC 202  
235 GAGTGATAGGAGTGGT---GAGACACACATATATGAGCTTTTCATATCCAGACTGA 291  
203 CAACCATATTAGTAGTGGTGGTGTACACCTACTTCCAGACAGTGTGAAGGGGGGATTC 262  
292 GCATCAGCAGGACAATTCGAAGAGCACTCTCTTTAAATGAACAGTCTCGAGCTA 351  
263 CCATCTCCAGAGACAATGCCAGAACCTCTGTACCTGCAATGAGCAGTCTGAGGTCTG 322  
352 CTGACACAGCATATATTACTGTGCCAATAATAGAGGGGATATTATATGATTTCATT 411  
323 AGGACAGGCCATGTTACTGTGCAAGAGCGGG-----GGACTCTATGA 367  
412 ATGCCATGGGACTACTGGGGTCAAGGAACCTCAGTACCGGTCTCTCAGCCAAACACAC 471  
368 TTACGACGGACTACTGGGGCAAGGACCACTCTCAGAGTCTCCTCAGCCAAACGACAC 427  
472 CCCCATCAGTCTATCCACTGCCCTCGGTGTGGAGATACAACTGGTTCCTCGGTGACTC 531  
428 CCCCATCTGTCTATCCACTGGCCCTGGATCTGTGCCAAACTAACTCCATGTGTGACCC 487  
532 TGGATGCTGCTCAAGGGTACTTCCCTGAGTCAGTCACTGTGACTTGGAACTCTGGAT 591  
488 TGGATGCTGCTCAAGGGTATTTCCTGAGCCAGTGACAGTCACTGGAACCTCTGGAT 547  
592 CCCGTCCAGCAGTGTGCACACCTTCCAGCTCTCCAGTCTGCTGCACTGTGACCTCTG 651  
548 CCCGTCCAGGGTGTGCACACCTTCCAGCTCTCCAGTCTGCTGCACTGTGACCTCTG 607  
652 GCAGCTCAGTGTGCTCCCTCCAGCAGCTGGCCAGTGCACAGCTGACCTGCACTGTG 711  
608 GCAGCTCAGTGTGCTCCCTCCAGCAGCTGGCCAGTGCACAGCTGACCTGCACTGTG 667  
712 CTCACCCAGCAGCAGCAGCAGCTGGTGCACAAACCTTGGCCAGCGGGGCCATTTCAA 771  
668 CCCACCCGGCCAGCAGCAGCAGCTGGTGCACAAACCTTGGCCAGCGGATGTGTGTGA 727  
772 CAATCAACCCCTGCTCCCTCAGCAGGAGTGTCAAAATGCCAGCTCTCAACCTCGAGG 831  
728 AGCCTTGCAATG-----TACAGTCCCGAG 751  
832 GTGACCACTCGCTCTCATCTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGA 891  
752 AAGTATCATCTGCTTCTCATCTCCCTCCAAAGCCCAAGGATGTGCTCACTTACTCTGA 811  
892 CACCAAGGTCAGTGTGTGGTGGATGTGAGCGAGGATGACCCAGCAGCTCCAGATCA 951  
812 CTCCTAAGGTCAGTGTGTGGTGGATGTGAGCGAGGATGATCCCGAGGTCCAGTTC 871  
952 GCTGTTTGTGAACAACTGGAAGTGTACACAGCTTCAGACACAAACCCCATAGAGAGATT 1011  
872 GCTGTTTGTAGATGATGTGAGGTGTACACAGCTTCAGACAAACCCCGGGAGGAGCAGT 931  
1012 ACAACAGTACTATCCGGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1071  
932 TCACAGCAGCTTTCGGCTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 991  
1072 GCAAGGATTCAAATGCAAGGTTCACACAAAGACTTCCCATCACCCTCCAGAGAACCA 1131  
992 GCAAGGATTCAAATGCAAGGTTCACACAAAGACTTCCCATCACCCTCCAGAGAACCA 1051  
1132 TCTCAAAATTAAGGGGTAGTTCAGAGTTCACAAAGTATACATCTTGGCCGCCAGCAGC 1191  
1052 TCTCAAAATTAAGGGGTAGTTCAGAGTTCACAAAGTATACATCTTGGCCGCCAGCAGC 1111  
1192 AGCAGTGTGTCAGGAAAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1251  
1112 AGCAGTGTGTCAGGAAAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1171  
1252 ACATCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1311

Db 1172 ACATTACTGTGGAGTGGCAGTGGGAATGGGCGAGCCAGCGAGAACTACAAGAACACTCAGC 1231  
QY 1312 CAGTCTGGAGTCTGACGGTCTTACTTATATATATAGCAAGCTCAATATGAAACAAGCA 1371  
Db 1232 CCATCATGGAGACAGATGGCTTACTTCTGCTACAGCAAGCTCAATGTGCAAGAGAGCA 1291  
QY 1372 AGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGACACAGAGGGTCTGAAAATTAAT 1431  
Db 1292 ACTGGGAGGAGGAATTAATTTACCTGCTCTGTGTATCATGAGGGCTGCACAACACC 1351  
QY 1432 ACCTGAAGAAGACCATCTCCGGTCTCCGGGTAAA 1466  
Db 1352 ATACTGAAGAAGCGCTCTCCACTCTCTCTGGTAAA 1386  
RESULT 10  
PCT-US02-35333A-21  
; Sequence 21, Application PC/TUS0235333A  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: Lohuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.0029P2  
; CURRENT APPLICATION NUMBER: PCT/US02/35333A  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 1386  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
; OTHER INFORMATION: Synthetic Construct  
PCT-US02-35333A-21

Query Match 42.2%; Score 670.6; DB 1; Length 1386;  
Best Local Similarity 69.4%; Pred. No. 1.8e-165;  
Matches 982; Conservative 0; Mismatches 379; Indels 54; Gaps 3;  
QY 55 TCTGCTGGTGACATTCCTCCAGCTGTGCTTATCCAGTGCAGCTGAGCAGTCCAGGAC 114  
Db 23 TTTCTCTGCTGCTCTTTTAAAGGTGCTCCAGTGTGAAGTGTGCTGCTGGAGCTGGGG 82  
QY 115 CTGGCTAGTGCAGCCCTCAGACAGCCCTGCTCCATCCTGACAGCTCTCTGCTTTCTCAT 174  
Db 83 GAGGCTTAGTGAAGCTGGAGGTCCTCCGAACTCTCTGTCAGCCCTCTGATTCACCT 142  
QY 175 TAACTAGTATGCTGTACACTGGGTTCGTTCAGTCTCCAGAAAGGCTCTGGAGTGGCTG 234  
Db 143 TCAGTAGTATGATGATGCTTGGGTTCGCCAGCTCCGAGAGAGGCTGGAGTGGGTG 202  
QY 235 GAGTATGATGAGTGGGTG---GAGACACAGACTATAATGACGCTTTATATCCAGCTGA 291  
Db 203 CAACCATTAGT 262  
QY 292 GCATCAGCAGGACAATTCCTCAAGAGCCTCTCTTTTAAATGACAGCTCTGCGAGCTA 351  
Db 263 CCATCTCCAGACAAATGCAAGAACCCCTGTACTGTCAATGAGCAGTCTGAGGTCTG 322  
QY 352 CTGACACAGCCATATATTACTGTGCGAGAAATAGGGGATATTTTACTATGATTTTCACTT 411

323 AGGACACGGCCATGTATTACTGTGCAAGCGGG-----GGACTCTATGA 367  
412 ATGCATGGACTACTTGGGGTCAAGAACTCAGTCACCGTCTCCCTCAGCAAAACACAC 471  
368 TTACGACGGACTACTTGGGGCAAGCAACCACTCTCACAGTCTCCTCAGCAAAACACAC 427  
472 CCCATCAGTCTATCCACTGGCCCTGGGTGGAGATACAACTGGTCTCCCTCGACTC 531  
428 CCCATCTGTCTATCCACTGGCCCTGGGTGGAGATACAACTGGTCTCCCTCGACTC 487  
532 TGGGATGCTGTCAAGGCTACTTCCCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 591  
488 TGGGATGCTGTCAAGGCTACTTCCCTGAGCAGTCAAGTCAAGTCAAGTCAAGT 547  
592 CCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCCTGAGTCTGAGTCTGAGTCTG 651  
548 CCCTGTCCAGGCTGTGCACACCTTCCAGCTCTCCTGAGTCTGAGTCTGAGTCTG 607  
652 GCAGTCACTGACTGTCCCTCCAGCACTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 711  
608 GCAGTCACTGACTGTCCCTCCAGCACTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 667  
712 CTCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 771  
668 CCCACCGGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 727  
772 CAATCAACCCCTGCTCCCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 831  
728 AGCCTTCATATG-----TACAGTCCACG 751  
832 GTGGACCATCGTCTTCATCTTCCCTCCAAATATCAAGGATGACTCATGCTCCCTGA 891  
752 AAGTATCATCTGTCTTCATCTTCCCTCCAAATATCAAGGATGACTCATGCTCCCTGA 811  
892 CACCAAGGTCACGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 951  
812 CTCCTAAGTTCACGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 871  
952 GCTGGTGGTGAACAACGTGGAGTACACAGTTCAGACAGTTCAGACAGTTCAGACAG 1011  
872 GCTGGTGGTGAACAACGTGGAGTTCAGACAGTTCAGACAGTTCAGACAGTTCAGACAG 931  
1012 ACAACAGTACTATCCGGTGTGACAGCCTTCCCTCCAGCAGCAGCAGCAGCAGCAGCAG 1071  
932 TCAACAGCAGTCTCCGCTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 991  
1072 GCAAGGATTCAAATCAAGTCAACAAGACCTCCCAATCAAGTCAAGTCAAGTCAAGTCA 1131  
992 GCAAGGATTCAAATCAAGTCAACAAGACCTCCCAATCAAGTCAAGTCAAGTCAAGTCA 1051  
1132 TCTCAAAATTAAGGGCTAGTCAAGCTCCCAAGTATACATCTTCCGCGCCACAGCAG 1191  
1052 TCTCAAAATTAAGGGCTAGTCAAGCTCCCAAGTATACATCTTCCGCGCCACAGCAG 1111  
1192 AGCAGTTGTCAGAAAGATGTCACTCTCACTTCCCTGGTGGTGGTGGTGGTGGTGGTGG 1251  
1112 AGCAGATGGCCAAAGTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1171  
1252 ACATCAGTGTGGAGTGACAGCAATGGGATACAGAGGAGAACTACAGGACACCCGAC 1311  
1172 ACATCAGTGTGGAGTGACAGCAATGGGATACAGAGGAGAACTACAGGACACCCGAC 1231  
1312 CAGTCCGAGTCTGACGGTCTTACCTTATATATACAGAGTCAATATGAAACAGCA 1371  
1232 CCATCAGTGGACAGATGGTCTTACCTTATATATACAGAGTCAATATGAAACAGCA 1291  
1372 AGTGGGAGAAACAGATTCCTCTCATGCAAGGTGACAGCAGGAGGCTGGAATAATTACT 1431  
1292 ACTGGGAGGAGAAATACCTTACCTGCTCTGTTTACATGAGGGCTGCACAAACACC 1351  
1432 ACCTGAGAGAGACCATCTCCGGTCTCCGGGTAAA 1466  
1352 ATACTGAGAGAGCCTCTCCCACTCTCTGGTAAA 1386

## RESULT 11

US-10-286-132A-21

; Sequence 21, Application US/10286132A

; GENERAL INFORMATION:

; APPLICANT: Zhou, Tong

; APPLICANT: Kimberly, Robert P.

; APPLICANT: Koopman, William J.

; APPLICANT: Lobuglio, Albert S.

; APPLICANT: Buchsbaum, Donald J.

; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF

; FILE REFERENCE: 21085.002907

; CURRENT APPLICATION NUMBER: US/10/286,132A

; PRIOR FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: US 60/346,402

; PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: PCT/US01/14151

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,344

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 21

; LENGTH: 1386

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:/Note - Synthetic Construct  
US-10-286-132A-21

Query Match 42.2%; Score 670.6; DB 9; Length 1386;

Best Local Similarity 69.4%; Pred. No. 1.8e-165;

Matches 982; Conservative 0; Mismatches 379; Indels 54; Gaps 3;

QY	55	TCTGCTGGTGCATATCCCAAGCTGTGCTCTATCCAGTGCAGTGAAGCAGTCAAGCAG	114
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QY	115	CTGCGCTAGTGCAGCCCTCAGACAGCCTGTCCATCACCTGCACAGTCTCTGTTTCTCAT	174
Db	83	GAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCTGTGCAGCCTCTGGATTCACTT	142
QY	175	TAACTAGTATATGTGTACACTGGGTTCGTGCTCAGTCTCCAGGAAGGTCTGGAGTGGCTGG	234
Db	143	TCAGTAGTATGTATGTCTTGGGTTCAGCAGTCCCGAGAGAGGCTGGAGTGGGTGG	202
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QY	292	GCATCAGCAAGCAATTCGAAGCCAACTCTCTTTAAATGAACAGTCTGCGAGCTA	351
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QY	412	ATGCCATGCACTACTGGGTCAAGGAACCTCAGTCAACGCTCTCTCAGCCAAAACACAC	471
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; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van de Vijver, Laura Johanna  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
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; PRIOR FILING DATE: 2002-06-14  
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; US-10-342-887-1932

Query Match 40.5%; Score 643.6; DB 9; Length 1673;  
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Y 148 GAGCGTGGTCCAGCCTGGGAGTCTCTGAGACTCTCTGTGCAAGCTCTGGATTCACT 207  
b 175 TAAGTATGATGTTACAGTGGTTCGTAGTCTCCAGGAAAGGCTGAGTGGCTGG 234  
Y 208 TCAGTAATATGATGATGCTGCTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGG 267  
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GenCore version 5.1.6  
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US-09-770-916-1

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# SUMMARIES

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4	963	60.6	1645	3	US-07-904-074A-3 Sequence 3, Appli
5	940.8	59.2	1570	3	US-07-743-329-6 Sequence 6, Appli
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8	939.2	59.1	1570	17	US-09-348-224-6 Sequence 6, Appli
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## ALIGNMENTS

US01

-09-770-916-1

Sequence 1, Application US/09770916

GENERAL INFORMATION:

APPLICANT: Frank, Dara W.

APPLICANT: Wiener-Kronish, Jeannine

APPLICANT: Yahr, Timothy L.

APPLICANT: Sava, Teiji

TITLE OF INVENTION: Method of and compositions for immunization with the

TITLE OF INVENTION: pseudomonas V antigen

FILE REFERENCE: 650053.91487

CURRENT APPLICATION NUMBER: US/09/770,916

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 09/448,339

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: 60/109,952

PRIOR FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: 60/126,794

PRIOR FILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patent in Ver. 2.1

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QY 181 GCTATGGTGACATTCCTCCAGGTCCTGCTCAGTCTCCAGAAAGGCTCTGGAGTGGGAGTGA 240

Db 181 GCTATGGTGACATTCCTCCAGGTCCTGCTCAGTCTCCAGAAAGGCTCTGGAGTGGGAGTGA 240

QY 241 TATGAGTGGTGAGACACAGACTATATGAGCTTTCATATCCAGACTGAGCATCAGCA 300

Db 241 TATGAGTGGTGAGACACAGACTATATGAGCTTTCATATCCAGACTGAGCATCAGCA 300

QY 301 AGGACAATTCCTCCAGGTCCTCTTTAAATGAACAGCTCTGAGCTACTGACACAG 360

Db 301 AGGACAATTCCTCCAGGTCCTCTTTAAATGAACAGCTCTGAGCTACTGACACAG 360

QY 361 CCATATATTACTGTGCCAGAAATAGAGGGGATTTACTATGATTTCACTTATGCCATGG 420

Db 361 CCATATATTACTGTGCCAGAAATAGAGGGGATTTACTATGATTTCACTTATGCCATGG 420

QY 421 ACTACTGGGGTCAAGGACCTCAGTCACCGTCTCTCAGCCAAACACACCCCATCAG 480

Db 421 ACTACTGGGGTCAAGGACCTCAGTCACCGTCTCTCAGCCAAACACACCCCATCAG 480

QY 481 TCTATCCACTGGCCCTGGGTGTGGAGATACAACTGGTTCTCCGTGACTCTGGGATGCC 540

Db 481 TCTATCCACTGGCCCTGGGTGTGGAGATACAACTGGTTCTCCGTGACTCTGGGATGCC 540

QY 541 TGGTCAAGGGTACTTCCCTGAGTCAGTCAGTGTGGAACCTCTGGATCCCTGTGCA 600

Db 541 TGGTCAAGGGTACTTCCCTGAGTCAGTCAGTGTGGAACCTCTGGATCCCTGTGCA 600

QY 601 GCAGTGTGCACACCTTCCAGCTCTCCCTGAGTCTGGACTCTACACTATGAGCAGCTCAG 660

Db 601 GCAGTGTGCACACCTTCCAGCTCTCCCTGAGTCTGGACTCTACACTATGAGCAGCTCAG 660

QY 661 TGACTGTCCCTCCAGCAGCTGGCCAAAGTCAGCAGCTCAGCTGAGCGTTGCTCAGCCAG 720

Db 661 TGACTGTCCCTCCAGCAGCTGGCCAAAGTCAGCAGCTCAGCTGAGCGTTGCTCAGCCAG 720

QY 721 CCAGCAGCAGCAGCTGGGACAAAACCTTGAGCCAGCGGGGCCCATTTCAACAATCAACC 780

Db 721 CCAGCAGCAGCAGCTGGGACAAAACCTTGAGCCAGCGGGGCCCATTTCAACAATCAACC 780

QY 781 CCTGTCTTCCATGCAAGGAGTGTCAAAATGCCAGCTCCCTAACCTCGAGGTTGACCAT 840

Db 781 CCTGTCTTCCATGCAAGGAGTGTCAAAATGCCAGCTCCCTAACCTCGAGGTTGACCAT 840

QY 841 CCGTCTTCTATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAGG 900

841 CCGCTTTCATCTCCCTCAATATCAAGGATGTACTCATGATCTCCCTGACACCAAGG 900  
901 TCACGTGTGTGGTGTGATGTGAGCGAGGATGACCCAGAGCTCCAGATCAGCTGTTG 960  
901 TCACGTGTGTGGTGTGATGTGAGCGAGGATGACCCAGAGCTCCAGATCAGCTGTTG 960  
961 TGAACAAGCTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTA 1020  
961 TGAACAAGCTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTA 1020  
1021 CTATCCGGGTGGTGTGATGTGAGCGAGGATGACCCAGAGCTCCAGATCAGCTGTTG 1080  
1021 CTATCCGGGTGGTGTGATGTGAGCGAGGATGACCCAGAGCTCCAGATCAGCTGTTG 1080  
1081 TCAATGCAAGGTCAACAAACAAAGACCTCCCATCAGAGAGATTACACAGTA 1140  
1081 TCAATGCAAGGTCAACAAACAAAGACCTCCCATCAGAGAGATTACACAGTA 1140  
1141 TTAAGGGCTAGTCAGAGCTCCCAAGATATACATCTTCCGCGCCACGACAGAGATTGT 1200  
1141 TTAAGGGCTAGTCAGAGCTCCCAAGATATACATCTTCCGCGCCACGACAGAGATTGT 1200  
1201 CCAGGAAGATGTGATGTGATGTGAGCGAGGATGACCCAGAGCTCCAGATCAGCTG 1260  
1201 CCAGGAAGATGTGATGTGATGTGAGCGAGGATGACCCAGAGCTCCAGATCAGCTG 1260  
1261 TGGAGTGACCAAGCAATGGGCATACAGAGGAGAACTACAAGGACACCCAGCTCTGG 1320  
1261 TGGAGTGACCAAGCAATGGGCATACAGAGGAGAACTACAAGGACACCCAGCTCTGG 1320  
1321 ACTGTGAGCTTCTTACTTATATAGCAAGCTCAATATGAAACAAAGCAAGTGGGAGA 1380  
1321 ACTGTGAGCTTCTTACTTATATAGCAAGCTCAATATGAAACAAAGCAAGTGGGAGA 1380  
1381 AAACAGATTCCTTCTGATGCAAGCTGACAGAGGAGTCTGAAACAAAGCAAGTGGGAGA 1440  
1381 AAACAGATTCCTTCTGATGCAAGCTGACAGAGGAGTCTGAAACAAAGCAAGTGGGAGA 1440  
1441 AGACCATCTCCGCTCTCCGGGTAAATGAGCTCAGACACCCCAAGCTCTCAGGTCCTAA 1500  
1441 AGACCATCTCCGCTCTCCGGGTAAATGAGCTCAGACACCCCAAGCTCTCAGGTCCTAA 1500  
1501 GAGACTGACCAAGCTATCCATCATCCCTTGTATATAAAGCATCCAGCAAGCTG 1560  
1501 GAGACTGACCAAGCTATCCATCATCCCTTGTATATAAAGCATCCAGCAAGCTG 1560  
1561 GTACCATGTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1588  
1561 GTACCATGTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1588

## RESULT 2

US-09-653-755A-3

Sequence 3, Application US/09653755A

## GENERAL INFORMATION:

APPLICANT: Eisinger, Dominic P.

APPLICANT: Stiles, Lynn

APPLICANT: Lamarche, Arthur

APPLICANT: Jelinek, Thomas

TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for

TITLE OF INVENTION: Phosphotyrosine-Containing Proteins

FILE REFERENCE: 724650-3

CURRENT APPLICATION NUMBER: US/09/653,755A

CURRENT FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 1389

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: cDNA for heavy

; OTHER INFORMATION: chain of recombinant antibody with 3'-histidine  
; OTHER INFORMATION: tag sequence  
US-09-653-755A-3

Query Match 68.3%; Score 1084; DB 25; Length 1389;

Best Local Similarity 87.2%; Pred. No. 1.1e-255;

Matches 1218; Conservative 1; Mismatches 156; Indels 21; Gaps 2;

QY 91 AGTGCAGCTGAAGCAGTACAGGACCTGGCTAGTGCAGCCCTCAGAGCCCTGTCATCA 150  
Db 2 AGTGCAGCTGAAGCAGTACAGGACCTGGCTAGTGCAGCCCTCAGAGCCCTGTCATCA 61  
QY 151 COTGACAGCTCTCTGTTCTCATTAACCTAGCTATGGTGTACACCTGGGTTCGTCAGTCTC 210  
Db 62 COTGACAGCTCTCTGTTCTCATTAACCTAGCTATGGTGTACACCTGGGTTCGTCAGTCTC 210  
QY 211 CAGGAAGGCTGTGGAGCTGGGAGTATGGAGT---GGTGGAGACACAGATATA 267  
Db 122 ATGAGAGAGAGCTTCTGAGTGGATTGGAGGTATTAATCTTACTATGGTGTCTATCTTCA 181  
QY 268 ATGAGCTTTTATATCCAGACTGAGCATCAGCAAGGACAAATTCAGAGCCAACTTTCT 327  
Db 182 GCCCGAAGTTCAAGGCAAGGCAATTTGACTGTAGACAAGTCTCCAGCAGCAGCTACA 241  
QY 328 TTAATGAACAGTCTGCGAGCTACTGACACAGCATATATATTACTGTGCCAGAAATAGAG 387  
Db 242 TGGAGCTCCGACGCTGACATCTGAGGATTTCTGCACTTATTTACTGTGCAAGAAGGGTG 301  
QY 388 GGGATATTTACTATGATTTCATCTTATGCACTGAGTACTGAGGTCAAGGAACCTCAGTCA 447  
Db 302 GGG-----CGTACTACTTTGAGTACTGAGGCGCAAGGCAAGCAGCTCTCA 343  
QY 448 CCGTCTCTCAGCCAAAACACACCCCATCATGCTATCTCACTGGCCCTGGGTGGAG 507  
Db 344 CAGTCTCTCAGCCAAAACACACCCCATCATGCTATCTCACTGGCCCTGGGTGGAG 403  
QY 508 ATACAACCTGGTTCCTCCGCTGACTCTGGGATGCTGCTCAAGGGCTACTTCCCTGAGTCA 567  
Db 404 ATACAACCTGGTTCCTCCGCTGACTCTGGGATGCTGCTCAAGGGCTACTTCCCTGAGTCA 463  
QY 568 TGACGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACTTCCAGCTCTCC 627  
Db 464 TGACGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACTTCCAGCTCTCC 523  
QY 628 TGCAGCTGGAAGCTTACACTATGAGCAGCTCAGTCTGCTCCCTCCAGCAGCTGGCCAA 587  
Db 524 TGCAGCTGGAAGCTTACACTATGAGCAGCTCAGTCTGCTCCCTCCAGCAGCTGGCCAA 583  
QY 688 GTGACACCTGACCTGACGCTTGGCTCACCAGCCAGCAGCAGCAGCTGGGACAAAAC 747  
Db 584 GTGACACCTGACCTGACGCTTGGCTCACCAGCCAGCAGCAGCAGCTGGGACAAAAC 643  
QY 748 TTGAGCCAGCGGGCCCATTTCAACATCAACCCCTGCTCCATGCAAGGAGTGTCA 807  
Db 644 TTGAGCCAGCGGGCCCATTTCAACATCAACCCCTGCTCCATGCAAGGAGTGTCA 703  
QY 808 AATGCCAGCTCTTAACCTCGAGGCTGAGCACTCCGCTCTTCTATCTTCCCTTCAATATCA 867  
Db 704 AATGCCAGCTCTTAACCTCGAGGCTGAGCACTCCGCTCTTCTATCTTCCCTTCAATATCA 763  
QY 868 AGGATGTACTCATGATCTCCCTGACACCCAGGTCACCTGTGTGGTGGTGGTGGAGCG 927  
Db 764 AGGATGTACTCATGATCTCCCTGACACCCAGGTCACCTGTGTGGTGGTGGTGGAGCG 823  
QY 928 AGGATGACCCAGAGCTCCAGATCAGCTGTTGTGAAACAAGTGAAGTACACAGCTC 987  
Db 824 AGGATGACCCAGAGCTCCAGATCAGCTGTTGTGAAACAAGTGAAGTACACAGCTC 883  
QY 988 AGACACAAACCCATAGAGAGGATTACACAGTACTATCCGGGTGTGTCAGCAGCTCCCA 1047  
Db 884 AGACACAAACCCATAGAGAGGATTACACAGTACTATCCGGGTGTGTCAGCAGCTCCCA 943  
QY 1048 TCCAGCAGCAGGAGCTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACAAAGACC 1107

944 TCCAGCACCAGGACTGGATGAGTGGCAAGAGTTCAATGCAAGGTCAACAACAGACC 1003  
1108 TCCCATCACCACATCGAGAGAACCATCTCAAAAAATTAAGGGCTAGTCAGAGCTCCACAAG 1167  
1004 TCCCATCACCACATCGAGAGAACCATCTCAAAAAATTAAGGGCTAGTCAGAGCTCCACAAG 1063  
1168 TATACATCTTTCGGCCACCAGCAGAGCAGTTGTCCAGGAAGATGTCAGTCTCACTTGGC 1227  
1064 TATACATCTTTCGGCCACCAGCAGAGCAGTTGTCCAGGAAGATGTCAGTCTCACTTGGC 1123  
1228 TGGTCGTGGGCTTCAACCCCTGGAGACATCAGTGTGGAGTGGAGCAAAATGGGCATACAG 1287  
1124 TGGTCGTGGGCTTCAACCCCTGGAGACATCAGTGTGGAGTGGAGCAAAATGGGCATACAG 1183  
1288 AGGAGAACTACAAGGACACCGCAGCTCTGGACTCTGAGGTTCTTACTTCAATATATA 1347  
1184 AGGAGAACTACAAGGACACCGCAGCTCTGGACTCTGAGGTTCTTACTTCAATATATA 1243  
1348 GCAAGCTCAATATGAAACAAAGCAAGTGGGAGAAACAGATTCCTTCTCATGCAACGTGA 1407  
1244 GCAAGCTCAATATGAAACAAAGCAAGTGGGAGAAACAGATTCCTTCTCATGCAACGTGA 1303  
1408 GACACGAGGCTGAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1467  
1304 GACACGAGGCTGAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1363  
1468 GAGCTCAGCACCACCA 1483  
1364 GTGGCCATCACCCCA 1379

Sequence 1, Application US/09653755A  
GENERAL INFORMATION:  
APPLICANT: Eisinger, Dominic P.  
APPLICANT: Stiles, Lynn  
APPLICANT: Lamarche, Arthur  
APPLICANT: Jelinek, Thomas  
TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for  
TITLE OF INVENTION: Phosphotyrosine-Containing Proteins  
FILE REFERENCE: 724650-3  
CURRENT APPLICATION NUMBER: US/09/653,755A  
CURRENT FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1365  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cDNA for heavy  
OTHER INFORMATION: chain of recombinant antibody

--09-653-755A-1

Query Match 68.1%; Score 1081.2; DB 25; Length 1365;  
Best Local Similarity 87.6%; Pred. No. 5,1e-255;  
Matches 1211; Conservative 1; Mismatches 149; Indels 21; Gaps 2;

91 AGGTGACGCTGAAGCAGTCAGAGCCTGGCCCTAGTCAGACCCCTCAGACAGCCTGTCCATCA 150  
2 AGGTCCAGCTGCARAGCTGGACCTGAAGCTGGTGAAGCCTGGGGCTTCAGTGTATGATAT 61  
151 CTGCACAGCTCTCGGTTTCATTAATAGTATGTTGTACACTGGCTTGTGTCAGTCTC 210  
62 CTGCAGGACTTCTGCATACACATCTCACTGAAACACCGCTGCATCGGCTGAAGCAGGCC 121  
211 CAGGAAGGGCTGAGTGGCTGGAGTATGGAGT---GGTGGAGACACAGACTATA 267  
122 ATGGAGAGGCTTGTGAGTGGATGGAGTATTAATCCTTACTATGTTGGTGTCTATCTTCA 181  
268 ATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCGAAGCAACCACTCTTCT 327

182 GCCGAAGTTCAAGGGCAAGGCCACATTTGACTGTAGACAAGTCTCTCCAGCACAGCCTACA 241  
328 TTAATAATGAACAGTCTGGAGCTACTGACACAGCCATATATTACTGTGCCAGAAATAGAG 387  
242 TGGAGCTCCGCGAGCCTGACATCTGAGGATTTCTGAGTCTATTACTGTGCAAGAAAGGGTG 301  
388 GGGATATTTACTATGATTTCACTTATGCCATGGGACTACTGGGTCACAGGAACCTCAGTCA 447  
302 GGG-----CGTACTACTTTGACTACTGGGGCCAAAGGCCACTCTCTCA 343  
448 CCGTCTCTCAGCCCAAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAG 507  
344 CAGTCTCTCAGCCCAAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAG 403  
508 ATACAACCTGGTTCCTCGGTGACTCTGGGATGCTGGTCAAGGGTACTTCCCTGAGTCAAG 567  
404 ATACAACCTGGTTCCTCGGTGACTCTGGGATGCTGGTCAAGGGTACTTCCCTGAGTCAAG 463  
568 TGACTGTGACTTGGAACTCTGGATCCCTGTCCAGAGTGTGCACACCTTCCAGCTCTCC 627  
464 TGACTGTGACTTGGAACTCTGGATCCCTGTCCAGAGTGTGCACACCTTCCAGCTCTCC 523  
628 TGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGTCTCCCTCCAGACCTTGGCCCAA 687  
524 TGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGTCTCCCTCCAGACCTTGGCCCAA 583  
688 GTACAGCGCTCACCTGACGCTTGTCTCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 747  
584 GTACAGCGCTCACCTGACGCTTGTCTCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 643  
748 TTGAGCCCGAGCGGGCCCATTTCAACAATCAACCCCTGTCTCCATGCAAGGAGTGTCA 807  
644 TTGAGCCCGAGCGGGCCCATTTCAACAATCAACCCCTGTCTCCATGCAAGGAGTGTCA 703  
808 AATGCCAGCTCTCAACCTCGAGGTTGACCATCGGTTCTTCTTCTTCTTCTTCTTCTTCTT 867  
704 AATGCCAGCTCTCAACCTCGAGGTTGACCATCGGTTCTTCTTCTTCTTCTTCTTCTTCTT 763  
868 AGGATGTACTCATGATCTCCCTGACACCCCAAGGTGACGTGTGTGTGTGTGTGTGTGTGTG 927  
764 AGGATGTACTCATGATCTCCCTGACACCCCAAGGTGACGTGTGTGTGTGTGTGTGTGTGTG 823  
928 AGGATGACCCAGAGCTCCAGATCAGCTGTTTGTGAACAACGTGGAAGTACACAGCTC 987  
824 AGGATGACCCAGAGCTCCAGATCAGCTGTTTGTGAACAACGTGGAAGTACACAGCTC 883  
988 AGACACAAACCCATAGAGAGGATTAACAACAGTACTATCCGGGTGTGACAGCCTTCCCA 1047  
884 AGACACAAACCCATAGAGAGGATTAACAACAGTACTATCCGGGTGTGACAGCCTTCCCA 943  
1048 TCCAGCACCAGCTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACAACAGACC 1107  
944 TCCAGCACCAGCTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACAACAGACC 1003  
1108 TCCATCATCCCATCCAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGCTTCCACAAG 1167  
1004 TCCATCATCCCATCCAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGCTTCCACAAG 1063  
1168 TATACATCTTTCGGCCACCAGCAGAGCAGTTGTCCAGGAAGATGTCAGTCTCACTTGGC 1227  
1064 TATACATCTTTCGGCCACCAGCAGAGCAGTTGTCCAGGAAGATGTCAGTCTCACTTGGC 1123  
1228 TGGTCTGGGCTTCAACCCCTGGAGACATCAGTGTGGAGTGGAGCAAAATGGGCATACAG 1287  
1124 TGGTCTGGGCTTCAACCCCTGGAGACATCAGTGTGGAGTGGAGCAAAATGGGCATACAG 1183  
1288 AGGAGAACTACAAGGACACCGCAGCTCTGGACTCTGAGGTTCTTACTTCAATATATA 1347  
1184 AGGAGAACTACAAGGACACCGCAGCTCTGGACTCTGAGGTTCTTACTTCAATATATA 1243  
1348 GCAAGCTCAATATGAAACAAAGCAAGTGGGAGAAACAGATTCCTTCTCATGCAACGTGA 1407



Db 1244 GCAGCTCAATATGAAACACAGCAAGTGGGAGAAAACAGATCTCTTCATGCAACGTGA 1303  
QY 1408 GACACGAGGGTCTGAAAAATTAACCTACCTGAAGAAGACCATCTCCGGGTCTCCGGGTAAAT 1467  
Db 1304 GACACGAGGGTCTGAAAAATTAACCTACCTGAAGAAGACCATCTCCGGGTCTCCGGGTAAAT 1363  
QY 1468 GA 1469  
Db 1364 GA 1365

## RESULT 4

JS-07-904-074A-3  
: Sequence 3, Application US/07904074A  
: GENERAL INFORMATION:  
: APPLICANT: John E. Shively  
: APPLICANT: Rainer Fischer  
: APPLICANT: Anna Wu  
: APPLICANT: Roy Paxton  
: APPLICANT: Y.H. Joy Yang  
: TITLE OF INVENTION: Chimeric Anti-CEA Antibody  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: City of Hope  
: STREET: 1500 East Duarte Road  
: CITY: Duarte  
: STATE: California  
: COUNTRY: United States of America  
: ZIP: 91010-0269  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3M Double Density 5 1/4" diskette  
: COMPUTER: Wang PC  
: OPERATING SYSTEM: MS-DOS (R) Version 3.30  
: SOFTWARE: Microsoft (R)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/904,074A  
: FILING DATE: 19920615  
: CLASSIFICATION: 530

PRIOR APPLICATION DATA: None  
ATTORNEY/AGENT INFORMATION:  
NAME: Irons, Edward S.  
REGISTRATION NUMBER: 16,541  
REFERENCE/DOCKET NUMBER: None  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 785-6938  
TELEFAX: (202) 785-5351  
TELEX: 440087 LM WSH  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1645  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Single Stranded  
TOPOLOGY: Unknown  
MOLECULE TYPE: Nucleic Acid  
HYPOTHETICAL: Not Applicable  
ANTI-SENSE: Not Applicable  
FRAGMENT TYPE: Not Applicable  
ORIGINAL SOURCE: Synthetically Prepared  
IMMEDIATE SOURCE: Synthetically Prepared  
POSITION IN GENOME: None  
FEATURE: None  
PUBLICATION INFORMATION: None

## JS-07-904-074A-3

Query Match 60.6%; Score 963; DB 3; Length 1645;  
Best Local Similarity 77.6%; Pred. No. 6.8e-226;  
Matches 1215; Conservative 0; Mismatches 320; Indels 30; Gaps 3;

QY 24 CATCAGAGCATGGCTGCTCTTCTGGGCTGCTCTTCTGCTGGTGGACATTCCTCAAGCTGTCTC 83  
Db 70 CACCTCACCATGAACCTTCGGGCTTCAGCCTGATTTCTCTGCTTGTCTTGTAAAGGTGTC 129  
QY 84 CTATCCAGGTGACGCTGAAGCAGCTAGGACCTGGCCTAGTGGACCCCTCACAGGCCTG 143

Db 130 CAGTGTGAAGTCAAGCTGGTGGAGTCTGGGGAGGCTTTGTGAAGCCTCGAGGGTCCCTG 189  
QY 144 TCATCACTACCTGCACAGTCTCTGGTTCCTCAATTAACCTAGCTATGGGTGTACACTGGGTCTGT 203  
Db 190 AAACCTCTCTCTGGCAGCCTCCGGATTCACTTCAGTAGTATATGCCATCTCTCTGGGTCTGC 249  
QY 204 CAGTCTCCAGGAAAGGCTGCTGGAGTGGCTGGGAGTGCATATGAGTGGTGGAGACACAGAC 263  
Db 250 CAGACTCCAGAGAAGAGGCTGGAGTGGTGGCATCCATTAGTAGTGGTATACACTTC 309  
QY 264 TATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGCACAATTCACAGGCCAACTC 323  
Db 310 TATGTAGACAGTGTGAAGGCCGATTCACCGTCTCCAGAGACAATGCCAGGACATCTCTG 369  
QY 324 TTTCTTTAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCCAGAAAT 383  
Db 370 TACCTGCAAAATGAGCAGTCTGAGGTCTGAGGACACGGCCATGATATTACTGTCAAGA --- 426  
QY 384 AGAGGGGATATTTACTATGATTTCACTTATGCGCATGGACTACTGGGTCAAGGACCTCA 443  
Db 427 -----ATCGACTACTACGAGGAGGGGATTTGGTTACTGGGGCCAAAGGACTCTG 477  
QY 444 GTCACCGTCTCTCAGCCAAACACACCCCATCAGTCTATCATCTATCCACTGCCCTCTGGGT 503  
Db 478 GCCACTGTCTGCGAGCCAAACACAGCCCATCGGTCTATCCACTGGCCCTCTGTGT 537  
QY 504 GGAGATCAAACTGGTTCCTCGTGACTCTGGGAGTCTGGTCTCAAGGGCTACTTCCCTGAG 563  
Db 538 GGAGATCAAACTGGTTCCTCGTGACTCTAGGATGCTGGTCTCAAGGGTATTTCCTGAG 597  
QY 564 TCAGTACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCT 623  
Db 598 CCAGTGAACCTTGAACCTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCAGCT 657  
QY 624 CTCTGCGAGTCTGAGTCTACACTATGAGCAGCTCAGTGTCTCCCTCCAGCAGCTGG 683  
Db 658 GTCTGCGAGTCTGAGTCTACACCTCTCAGCAGCTCAGTGTAACTCGAGACCTGG 717  
QY 684 CCAAGTCAGACGCTCACTGCGAGCGTCTGTCACCCAGCAGCAGCAGCAGCAGGTCGACAAA 743  
Db 718 CCCAGCAGTCCATCACTGCAATGTGGCCACCCGGAAGCAGCAGCAGGTCGACAA 777  
QY 744 AAATTTAGCCCGAGGGCCCATTTCAACAACTCAACCCCTGTCTCTCCATGCAAGGAGTGT 803  
Db 778 AAATTTAGCCCGAGGGCCCATTTCAACAACTCAACCCCTGTCTCTCCATG----- 821  
QY 804 CACAAATCCCGAGCTCTTAACCTCGAGGGTGGACCATCCGCTCTTCATCTTCCCTCCAAAT 863  
Db 822 --CAAAATCCCGAGCAGCTTAACCTCTTGGTGGACCATCCGCTCTTCATCTTCCCTCCAAAG 879  
QY 864 ATCAAGGATGTACTCATGATCTCCCTGACACCCAAAGTCAAGTGTGTGGTGGTGGATGTG 923  
Db 880 ATCAAGGATGTACTCATGATCTCCCTGAGCCCATAGTCACATGTGTGGTGGTGGATGTG 939  
QY 924 AGCGAGGATGACCCAGAGTCCAGATCAGCTAGCTGGTTGTGACACAGCTGGAAGTACACACA 983  
Db 940 AGCGAGGATGACCCAGAGTCCAGATCAGCTAGCTGGTTGTGAAACAGCTGGAAGTACACACA 999  
QY 984 GCTCAGACACAAACCCATAGAGAGATTACACAGTACTATCCGGGTGGTGGTGGTGGTGGTGGT 1043  
Db 1000 GCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTGGTGGTGGTGGTGGT 1059  
QY 1044 CCCATCCAGCAGCAGGACTGGATGGTGGCAGGAGTTCAATGCAAGGTCAACAAACAAA 1103  
Db 1060 CCCATCCAGCAGCAGGACTGGATGGTGGCAGGAGTTCAATGCAAGGTCAACAAACAAA 1119  
QY 1104 GACTCCCATCACCCTATCGAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGCTCCA 1163  
Db 1120 GACTCCCATCACCCTATCGAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGCTCCA 1179  
QY 1164 CAAGTATACATCTTGGCGCCACAGCAGCAGGAGTGTCCAGGAAAGATGTGAGTGTCTCACT 1223

1180 CAGGTATATGCTTTCCTCCACCAAGAGAGTACTAAGAAACAGGTCTCCTGACC 1239  
1224 TGCTGGTGTGGGCTTCAACCCCTGGAGACATCATGTGGAGTGGACACAGCAATGGGGCAT 1283  
1240 TGCATGGTTCACAGACTTTCATGCTGAAGACATTTACGTGGAGTGGACCAACAAGGGAAA 1299  
1284 ACAGAGGAACTACAGGACACCGCACCAGTCTCTGGACTCTGACGGTTCCTTACTTCATA 1343  
1300 ACAGAGCTAAACTCAAGAACACTGAACCACTCTGAGTCTGAGTCTTACTTTCATG 1359  
1344 TATACGACGCTCAATATGAAACAGCAAGTGGGAGAAACAGATTCTCTCATGCAAC 1403  
1360 TACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTCA 1419  
1404 GTGAGACAGGAGGTCTCAAAATTTACTACCTGAAAGAGAGACATCTCCCGGTCTCCGGGT 1463  
1420 GTGGTCCAGAGGGTCTGCACATTTACACAGGACTAAGAGCTTCTCCGGGACTCCGGGT 1479  
1464 AATGAGCTCAGACACCCCAAAAGCTCTCAGGTCTCTTAAGAGACACTGGCACCCATATCCAT 1523  
1480 AATGAGCTCAGACACCCCAAAAGCTCTCAGGTCTCAAGAGACACTGGCACCCATATCCAT 1539  
1524 GCATCCCTTGTATTAATTAAGCATCCAGCAAGCTGGTACCATGTAAACCAAAAAA 1583  
1540 GCTTCCCTTGTATTAATTAAGCAAGCAAGCAAGTGGGAGCAATGTAAGCAAAAAA 1599  
1584 AAAAA 1588  
1600 AAAAA 1604

## RESULT 5

Sequence 6, Application US/07743329

## GENERAL INFORMATION:

APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Emtage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/743,329  
FILING DATE: 19910917  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: CARP-0009

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439

## INFORMATION FOR SEQ ID NO: 6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1570 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA

## FEATURE:

NAME/KEY: CDS  
LOCATION: 41..1444

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 98..1444  
US-07-743-329-6

Query Match 59.2%; Score 940.8; DB 3; Length 1570;

Best Local Similarity 77.2%; Pred No. 1.9e-220;

Matches 1210; Conservative 0; Mismatches 322; Indels 36; Gaps 4;

QY 21 CTCCATCAGAGACTGGCTGTCTTGGGGCTGCTTCTTCTGCTGGTGCATATCCCAAGCTGT 80

DB 29 CTCGACTCAACATGGAAGGCACTGGATCTTCTTCTTCTGCTGGTGCATATCCCAAGCT 88

QY 81 GTCCATATCCAGGTCGAGCTGAAGCAGTCAGGACCTGGCCTAGTCAGCCCTCAGAGC 140

DB 89 GTCCATATCCAGGTCGAGCTGAAGCAGTCAGGACCTGGCCTAGTCAGCCCTCAGAGC 148

QY 141 CTGTCATCAGCTGCACAGTCTCTGGTTCCTCATTAAGTATGGTGTACACTGGGT 200

DB 149 GTGAAGATGTCTTCAAGGCTTCTGGCTACACCTTTACTAGTACACATGACCTGGGT 208

QY 201 CGTCAGTCTCCAGGAAAGGCTCTGGAGTGGCTGGGA---GTGATATGGAGTGGTGGAG 257

DB 209 AACAGAGGCTGGACAGGCTCTGGAATGGATGGATACATTAATCCTAGCGTGGTAT 268

QY 258 ACAGACTATAATGCAAGCTTTTCATATCCAGACTGAGCATCAGCAAGCAATTCACAGAG 317

DB 269 ACTAATTACATCAGAAGTTCAGAGGCAAGGCAACATGACTACAGACAAATCCTCCAGC 328

QY 318 CAACCTCTTTTAAATGAACAGTCTGGAGGCTACTGACACAGCCATATATTTACTGTGCC 377

DB 329 ACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCACTCTATTTACTGTGA 388

QY 378 AGAATAGAGGGATATTTACTATATTTCACTTATGCCATGACTACTGGGTCAAGGA 437

DB 389 AGA-----TATATGATGATATCTTATGCTTGGGCTGGGCTGGGCTGGGCTGGGCT 433

QY 438 ACCTCAGTCACCGTCTCTCAGCCAAACAAACACCCCATCATGCTATCCACTGGCCCT 497

DB 434 ACCACTCTCAGCTCTCTCAGCCAAACAAACACCCCATCATGCTATCCACTGGCCCT 493

QY 498 GGGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCTGGTGAAGGCTACTTTC 557

DB 494 GTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCTGGTGAAGGCTACTTTC 553

QY 558 COTGAGTCAGTGTGACTTGGAACTCTGGATCCCTGCTCCAGCAGTGTGCACACCTTC 617

DB 554 COTGAGTCAGTGTGACTTGGAACTCTGGATCCCTGCTCCAGCAGTGTGCACACCTTC 613

QY 618 CCAGCTCTCTCAGTGTGACTTACACTATGAGCAGCTCAGTGTGCTCCCTCCCTCCAGC 677

DB 614 CCAGCTCTCTCAGTGTGACTTACACTATGAGCAGCTCAGTGTGCTCCCTCCCTCCAGC 673

QY 678 ACCTGGCCAAAGTCAGACCTCAGTGTGCTCCCTCAGTGTGCTCCCTCAGTGTGCTCCCT 737

DB 674 ACCTGGCCAAAGTCAGACCTCAGTGTGCTCCCTCAGTGTGCTCCCTCAGTGTGCTCCCT 733

QY 738 GACAAAAAATTTGAGCCCAAGCGGCGCATTTCAACAATCAACCCCTGTCTCTCATGCAAG 797

DB 734 GACAAAAAATTTGAGCCCAAGCGGCGCATTTCAACAATCAACCCCTGTCTCTCATGCAAG 783

QY 798 GAGTGTCAAAATGGCCAGCTCTCAACCTCAGGCTGGAGGCTGGAGGCTGGAGGCTGGAG 857

DB 784 -----CAAAATGGCCAGCACTTAACTCTTGGGTGGAGGCTGGAGGCTGGAGGCTGGAG 835

QY 858 CCAATATCAAGGATCTACTCATGATCTCCCTGACACCCCAAGGTCACTGTGTGGTGGTG 917

DB 836 CCAAGATCAAGGATGATCATGATCTCCCTGAGCCCATAGTACATGTGTGGTGGTG 895

QY 918 GATGTGAGGAGGATGACCCAGCGTCCAGATCAGTGGTGTGGAACACGTTGGAAGTA 977

DB 896 GATGTGAGGAGGATGACCCAGCGTCCAGATCAGTGGTGTGGAACACGTTGGAAGTA 955



```

1 STREET: One Liberty Place - 46th Floor
2 CITY: Philadelphia
3 STATE: PA
4 COUNTRY: USA
5 ZIP: 19103
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patentin Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/485,686
15 FILING DATE: 07-JUN-1995
16 CLASSIFICATION: 424
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/743,329
20 FILING DATE: 17-SEP-1991
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Hohenschutz, Liza D.
23 REGISTRATION NUMBER: 33,712
24 REFERENCE/DOCKET NUMBER: CARP-0009
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (215) 568-3100
27 TELEFAX: (215) 568-3439
28 INFORMATION FOR SEQ ID NO: 6:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 1570 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: cDNA
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: 41..1444
38 FEATURE:
39 NAME/KEY: mat_peptide
40 LOCATION: 98..1444
41
42 CS-08-485-686-6

```

Query Match	59.2%;	Score	940.8;	DB	8;	Length	1570;	
Best Local Similarity	77.2%;	Pred.	No. 1.9e-220;					
Matches 1210;	Conservative	0;	Mismatches	322;	Indels	36;	Gaps	4;
QY	21	CTCCATCAGAGCATGCTGCTTTGGGGCTGCTCTTCTGCTTGCTGGTGCATATCCCAAGCTG	80					
Db	29	CTCTGACTCAACATGAAAGGCACTGGATCTTCTACTCTCTGTTGTTCAGTAACCTGCAGGT	88					
QY	81	GTCTTATCCAGGTGCAGCTGAAGCAGTCAGGACCTTGGGCTAGTGCAGCCCTCACAGAGC	140					
Db	89	GTCCACTCCCAGGTCCAGCTGCAGCAGTCGCGGCTGAACCTGGCAAGACCTGGGGCTCA	148					
QY	141	CTGTCCATCACCTGCACAGTCCTCTGTTTCTCATTAACTAGCTATGGTGTACACTGGTT	200					
Db	149	GTGAAGATCTCTGCAAGGCTTCTGGCTACACCTTTACTAGSTACAGATGCATGGGTA	208					
QY	201	CGTCAGTCTCCAGGAAGGCTCGGAGTGGCTGGGA--GTGATATGGAGTGGTGGAGAC	257					
Db	209	AAACAGGCGCTGGACAGGCTCTGGATGGATTGGATACATTAATCCTAGCCGTGGTTAT	268					
QY	258	ACAGACTATAATGCAGCTTTTCATATCCAGACTGAGCATCAGCAAGGACAATCCAGAGC	317					
Db	269	ACTAATACAAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAATCCTCCAGC	328					
QY	318	CAACTCTCTTTAAATGAACAGCTCTGCGAGCTACTGCACACAGCCATATATTACTGTGC	377					
Db	329	ACAGCCTACATGCAACTGAGCAGCCCTGCATCTGAGGACTCTGCAGTCTATTACTGTGCA	388					
QY	378	AGAAATAGAGGGGATATTTACTATTGATTTTCACTTATGCCATGGCACTACTGGGTCAAGGA	437					
Db	389	AGA-----TATTATGATGATTAATCTAGTCCCTTGACTACTGGGCCAAGGC	433					
QY	438	ACCTCAGTCACCGTCTCCTCAGGCCAAACACACCCCATCAGTCTATCATCTGGGCCCT	497					

738	GACAAAAAACTTGAGCCACAGGGGCCCAATTTCAACAATATCAACCCCTGTCTCTCATGCAAG	797
739		
743	GACAAGAAAATTTGAGCCACAGGGGCC-----ACAATCAAGCCCTGTCTCCTCATG-----	783
798	GAGTGTCACAAAATGCCAGCTCTCAACCTCGAGGCTGGACCATCCGCTCTCATCTTTCCCT	857
799		
784	-----CAAAATGCCAGACCTAACTCTTTGGGTGGACCATCCGCTCTCATCTTTCCCT	835
858	CCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCCAAGGTCAAGTGTGGTGGTG	917
859		
836	CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCATAGTCAACATGTGGTGGTG	895
918	GATGTAGCGAGGATGACCCAGACGCTCCAGATCAGCTGAGTGTGGTTGTGAACAACGTGGGAAGTA	977
919		
896	GATGTAGCGAGGATGACCCAGATCTCCAGATCAGCTGGTTGTGTGAACAACGTGGGAAGTA	955
978	CACACAGCTCAGACACAAACCATAGAGAGATTTACACAGTACTATCCGGGTGGTCAAGC	1037
979		
956	CACACAGCTCAGACACAAACCATAGAGAGATTTACACAGTACTCTCCGGGTGGTCAAGT	1015
1038	ACCTTCCCATCCAGACACGAGCTGGATGAGTGGCAAGGAGTTTCAATGCAAGGTCAAC	1097
1039		
1016	GCCTTCCCATCCAGACACGAGCTGGATGAGTGGCAAGGAGTTTCAATGCAAGGTCAAC	1075
1098	AACAAGACCTTCCCATCACCCATCGAGAGAACCATCTCAAAATTTAAAGGGCTAGTCAGA	1157
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1076	AACAAGACCTTCCAGCGCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGA	1135
1158	GCTCCACAGATATACATCTTTGGCGCCACAGCAGACGAGATTTGTCAGGAAGAGATGTCACT	1217
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1136	GCTCCACAGGATATGTCTTTGGCTCCACCAGAAGAGAGATGACTAAGAACAAGGTCACT	1195
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1278	GGGCATACAGAGAGAGAACTACAAGGACACCGACACGTCCTGGACTCTGACGGTCTTTAC	1337
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1256	GGGAAACACAGCTAAACTACAAGAACACTGAACACGTCCTGGACTCTGATGTTCTTTAC	1315
1338	TTCAATATATAGCAAGCTCAATATGAAAACACAGCAGTGGGAGAAAAACAGATTTCCTTCTCA	1397
1339		
1316	TTCAATGATACAGCAAGCTGAGGTGGAAAAGAAGAACTGGGTGGAAAAGAAATAGCTACTCC	1375
1398	TGCAACTGTGAGACACGAGGCTTGAAAAATTTACTACCTGGAAGAACCATCTCCCGGTCT	1457
1399		
1376	TGTTCAAGTGGTCCACGAGGCTGTGCAAAATACCACAGCTTAGAGCTTCTCCCGGACT	1435
1458	CCGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCTCTAAAGAGACACTGGCACCCCAT	1517
1459		
1436	CCGGTAAATGAGCTCAGCACCCACAAAACTCTCAGGTCCAAAGAGACACCCACACTCAT	1495
1518	ATCCATGCATCCCTTGTATATAATAAAGCATCOAGCAAAAGCCTGGTACCATGTAAAAAAA	1577
1519		
1496	CTCCATGCTCCCTTGTATATAATAAAGCACCCAGCAATGCCTGGGACCATGTAAAAAAA	1555
1578	AAAAAAA 1585	
1579		
1556	AAAAAAA 1563	

RESULT 7  
 :08-485-686-6  
 Sequence 6, Application US/08485686  
 GENERAL INFORMATION:  
   APPLICANT: Adair, John R.  
   APPLICANT: Athwal, Diljeet S.  
   APPLICANT: Emtage, John S.  
   TITLE OF INVENTION: Humanised Antibodies  
   NUMBER OF SEQUENCES: 28  
   CORRESPONDENCE ADDRESS:  
   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris

## RESULT 7







141 CTGTCCATACCTGCACAGCTCTCTGGTTTCTCATTAACCTAGCTATGCTGTACACTGGTT 200  
149 GTGAAGATGCTCTGAAGGCTCTGGCTACACCTTTACTAGGTACAGCATGCTAGCTGGTA 208  
201 CGTCAGTCTCCAGGAAGGCTCTGGAGTGGCTGGGA---GTGATATGGAGTGGTGGAGAC 257  
209 AAACAGAGGCTCGACAGGCTCTGGAATGGATGGATACATTAATCTAGCGTGGTTAT 268  
258 ACAGACTATATGACGCTTTCATATCCAGACTGAGCATGAGCAGGAGCAATTCACAGAGC 317  
269 ACTAATATACATTCAGAAGTTCAGAGCAAGGCCACATGTACTACAGACAAATCTCCAGC 328  
318 CAACCTCTCTTTAAATGAACAGTCTCGAGCTACTGACACAGCCATATATTAATCTGTGCC 377  
329 ACAGCCTACATGCAACTGAGCAGCTGACATCTGAGGACTCTGAGCTATTAATCTGTGCA 388  
378 AGAATAGAGGGGATATTTACTATGATTTTCACTTATGCCATGGACTACTGGGGTCAAGGA 437  
389 AGA-----TATTATGATGATCATTTACTGCTTGTACTACTGGGGCCAGGC 433  
438 ACCTCAGTCACCGTCTCTCAGCCAAACACACCCCATCAGTCTATCCACTGGCCCT 497  
434 ACCACTCTCAGAGTCTCTCAGCCAAACACACCCCATCGGTCTATCCACTGGCCCT 493  
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494 GTGTGTGGAGATACAACCTGCTTCCGTGACTTAGGATCGCTGCTCAAGGGTTATTTC 553  
558 CCTGAGTCAGTGTGACTGTGAACCTCTGGATCCCTGTCCAGAGGTGTCACACCTTC 617  
554 CCTGAGCCAGTGACTGTGACCTGGAACCTCTGGATCCCTGTCCAGTGGTGTGACACACCTTC 613  
618 CCAGCTCTCTGAGTGTGACTGTGACCTATGACACTATGACGCTCAGTACTGCTCCCTCCAGC 677  
614 CCAGCTGTCTGCTGCTGCTGCTGCTTACACCTCTCAGCAGCTCAGTACTGTAACTTCGAGC 673  
678 ACCTGGCCAACTGACAGCGTCACTGCGAGCTGTCTACCCAGCAGCAGCAGCAGCTGTG 737  
674 ACCGTGGCCAGCCAGTCTCCTCAGCTGCACTGTGGCCACCCGAGCAGCAGCAGCTGTG 733  
738 GACAAAAAATGTAGCCAGCGGCGCCATTTCAACAATCAACCCCTGTCTCCATGCAAG 797  
734 GACAGAAAAATGTAGCCAGAGGCGCC-----ACAATCAAGCCCTGTCTCCATG---- 783  
798 GAGTGTCAAAATGCCAGCTCTTAACCTCAGGCTGGACCATCGCTTTCATCTTCCT 857  
784 -----CAATGCCAGCAGCCTAACTCTTGGGTGGACCATCGCTTTCATCTTCCT 835  
858 CCAATATCAAGGATGTACTCATGATCTCCCTGACACCCCAAGTCACTGTGTGGTGTG 917  
836 CCAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCATAGTCAACATGTGTGGTGTG 895  
918 GATGTAGCGAGGATGACCCAGAGCTCCAGATCAGCTGTGTTGTGAACAACGTGAAGTA 977  
896 GATGTAGCGAGGATGACCCAGATGTCCAGATCAGCTGTGTTGTGAACAACGTGAAGTA 955  
978 CACAGAGCTCAGACACAACCCATAGAGAGGATTAACAACACTACTATCCGGGTGTGACG 1037  
956 CACAGAGCTCAGACACAACCCATAGAGAGGATTAACAACACTACTATCCGGGTGTGACG 1015  
1038 ACCCTCCCATCCAGCAGCAGGACTGTGATGAGTGGCAAGGAGTTCAATGCAAGGTCAAC 1097  
1016 GCCCTCCCATCCAGCAGCAGGACTGTGATGAGTGGCAAGGAGTTCAATGCAAGGTCAAC 1075  
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1076 AACAAAGACCTCCCATCAACCATCAGAGAACCATCTCAAAAATTAAGGGCTAGTCA 1135  
1158 GCTCCACAGTATACATCTTCCCGCCACCCAGCAGAGCAGTGTCCAGGAAGATCTCAGT 1217  
1136 GCTCCACAGTATGTCTTCCCTCCACAGGAAGAGATGACTTAAGAAACAGGTCACT 1195  
1218 CTCACCTTGCCTGGTGGGCTTCAACCTTGGAGACATCAGTGTGGAGTGGACCAAGCAAT 1277

1196 CTGACCTGCATGGTCACAGACTTTCATGCCTGAAGACATTTACGTGGAGTGGACCAAC 1255  
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1338 TTATATATAGCAAGCTCAATATGAAACAAAGCAAGTGGGAGAGAAACAGATTCCTTCTCA 1397  
1316 TTATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCC 1375  
1398 TGAACGTGACAGCAGGAGTCTGAAAATTTACTACCTGAAGAAAGACCATCTCCGGTCT 1457  
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1458 CCGGTAAATGAGCTCAGCAGCCACAAAGCTCTCAGGTCTCTAAGAGACACTGGACCCAT 1517  
1436 CCGGTAAATGAGCTCAGCAGCCACAAAGCTCTCAGGTCTCTAAGAGACACTGGACCCAT 1495  
1518 ATCATGCATCCCTTGTATAATAAAGCATCCAGAAAGCCTGTGATACCATGTAAAAAAA 1577  
1496 CTCATGCTTCCCTTGTATAATAAAGCAGCAGCAATGCTGGGACCATGTAAAAAAA 1555  
1578 AAAAAAA 1585  
1556 AAAAAAA 1563

## RESULT 11

US-09-795-515-6

; Sequence 6, Application US/09795515

; GENERAL INFORMATION:

; APPLICANT: Adair, John R.

; APPLICANT: Athwal, Diljeet S.

; APPLICANT: Emage, John S.

; TITLE OF INVENTION: Humanised Antibodies

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &amp; Norris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/795,515

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/846,658

; FILING DATE: 01-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Trujillo, Doreen Yanko

; REGISTRATION NUMBER: 35,719

; REFERENCE/DOCKET NUMBER: CARP-0057

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1570 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 41..1444





## CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/016,024

FILING DATE: 10-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Linker Jr., Raymond O.

REGISTRATION NUMBER: 26,419

REFERENCE/DOCKET NUMBER: 3339-177

TELEPHONE: 704-377-1561

TELEFAX: 704-334-2014

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1581 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 61..1467

FEATURE:

NAME/KEY: sig\_peptide

LOCATION: 61..117

LOCATION: 61..117

-08-462-767-1

Query Match

Best Local Similarity

Matches 1207; Conservative 0; Mismatches 335; Indels 33; Gaps 4;

9 TTCTCATAGAGCCTCCATCAGAGATGCTCTCTTGGGGCTGCTTCTTCTGCTGCTGACA 68

37 TTCTCTGAAGACACTGACTCTTAACATGGGATGGAGTGGATCTTCTTCTCTCTGTCA 96

69 TTCCCAAGCTGTCTTATCCAGGTGCGAGTGAAGCAGTGCAGGACCTGGCTTGTGCGAG 128

97 GGAAGTGCAGGTGCTCCATGCGAGTCCAGTGCAGCAGTCTGGACCTGAGCTGGTGAAG 156

129 CCCTCAGAGCCGTGTCATCAGCTGCAGTCTCTGTTCTCTATTAACAGTATGATGGT 188

157 CCAGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGCTACACCTTCACCTGACTACTAT 216

189 GTACACTGGTTCGCTCAGTCCAGGAAGGCTGAGAGTGGCTGGGAGTATGATGGAGT 248

217 ATAACTGGGTGAAGCAGAGACCTGGAGAGGACTTAAATGGATGGATGATTTATCCT 276

249 G- -GTGGAGACACAGACTAATATGACGCTTTTCATATCCAGACTGAGCATCAGCAAGGAC 305

277 GCAAGCGTAACTAAGTACATGAGAGACTTCAAGGCAAGGCCACATTGACTGTAGAC 336

306 AATTCCAAAGAGCCACTCTTCTTTAAATGAACAGTCTGCGAGCTACTGACACAGCCATA 365

337 ACATCTCCAGCAGCCTACATGCGAGCTCAGCAGCTGACATCTGAGGACACTGCTGTC 396

366 TATTACTGTGCGAGAAATAGAGGGATATTTACTATGATTTTCACTTATGCCATGCACTAC 425

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546 AAGGCTACTCTTCCCTGAGTCACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGT 605

565 AAGGCTTATTTCCCTGAGCAGTACCTTGAACCTCTGGATCCCTGTCCAGTGGT 624

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726 AGCACCAAGTGGGACAAAATTTGAGCCCAAGCGGCGCCATTTCAACAATCAACCCCTGT 785  
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847 TTATCTTCCCTCCAAATATCAAGATGTACTATGATCTCCCTGACACCAATGATACCA 906  
906 TGTGTGGTGGTGTGATGTCAGGAGATGATGAGGATGAGGATGATGATGATGATGATGAT 965  
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966 AACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTTACAACAGTACTATC 1025  
967 AACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTTACAACAGTACTATC 1026  
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1326 GAGGTTCTTACTTATATAGCAAGTCAATATGAAACCAAGCAAGTGGGAGGAGGAG 1385  
1327 GATGTTCTTACTTATGATGAGGAGTGGGAGGAGGAGTGGGAGGAGGAG 1386  
1386 GATGTTCTTACTTATGATGAGGAGTGGGAGGAGGAGTGGGAGGAGGAG 1445  
1387 AATAGTACTCTCTGTTAGTGTCCAGGAGTGTGCAATCACCACAGCTAAGAGC 1446  
1446 ATCTCCCGGTCTCCGGTAAATGAGTTCAGCACCAAGGAGTCTCAGGTTCTAAGAGAC 1505  
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1506 ACTGTCACCAATATCCATGATCCCTTGTATTAATTAAGCATCCAGCAAGCTGGTACC 1565  
1507 ACCCATCATCTCCATGCTTCCCTTGTATTAATTAAGCATCCAGCAAGCTGGTACC 1566  
1566 ATGTAATAAATAAATA 1580  
1567 ATGTAATAAATAAATA 1581

## RESULT 13

US-60-360-207-19352

; Sequence 19352, Application US/60360207

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF

; FILE REFERENCE: CL001321

Journal of Management Inquiry 26(4) 391-407 © The Author(s) 2017. Reprints and permissions: [sagepub.com/journalsPermissions.nav](http://sagepub.com/journalsPermissions.nav) DOI: 10.1177/1056492617710001

149 CACCTGCACAGTCTCTGGTTTCTCATTAAGTACCTATGGT

[illegible]

121 CACTTGCACTCTCTGGTGTTCAGTAACCAATATATGGTACACTGGGTTCGCCAGCC 180  
209 TCCAGGAAGGCTCGAGTGGCTGGAGTGATATATGGAGTGGTGAGACACAGACTATAA 268  
181 TCCAGGAAGGCTCGAGTGGCTGGAGTGAATATGGGCTGGTGAATACAAATATAA 240  
269 TGCAGCTTTTCATATCCAGACTGAGCATCAGCAAGCAAAATTCGAAGAGCCAACTCTCT 328  
241 TTCCGCTTTTCATATCCAGACTGAGCATCAGCAAGCAAAATTCGAAGAGCTCAAGTTTCT 300  
329 TAAATGAACAGTCTGGAGCTACTGACACAGCCATATATATGTCGCCAGAAATAGAGG 388  
301 AAAATGAACAGTCTGCAATGATGACACAGCCATGACTGTCGTCAGTCGCGGGGG 360  
389 GGATATTTACTATGATTTCACTTATGCACTGGACTGAGTGGGTCAAGGAACCTCAGTCAC 448  
361 -----TCACTACGGCTATGCTTTGGACTACTGGGTCAAGGAACCTCAGTCAC 408  
449 CGTCTCTCAGCAAAACACACCCCATCATCTATCTACCTGGCCCTGGGTGGAGA 508  
409 CGTCTCTCAGCTACACACAGCCCATCTGTCATCCCTGGTCCCTGGCTGCAGTGA 468  
509 TACAACCTGTTCCCTCGCTACTTGGGATGCTGGTCAAGGGCTACTTCCCTGAGTCACT 568  
469 CACATCTGGATCTCGGTGACACTGGGATGCTTGTCAAGGGCTACTTCCCTGAGCCGGT 528  
569 GACTGTGACTTGGAACTCTGATCTGCTGATGCTGCTGATGCTGCTGCTGCTGCT 628  
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589 GCAGTCTGGTCTATCTCCCTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648  
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709 CGAGCTAGATACCAAGCCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750  
809 ATGCCAGCTCTTAACCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868  
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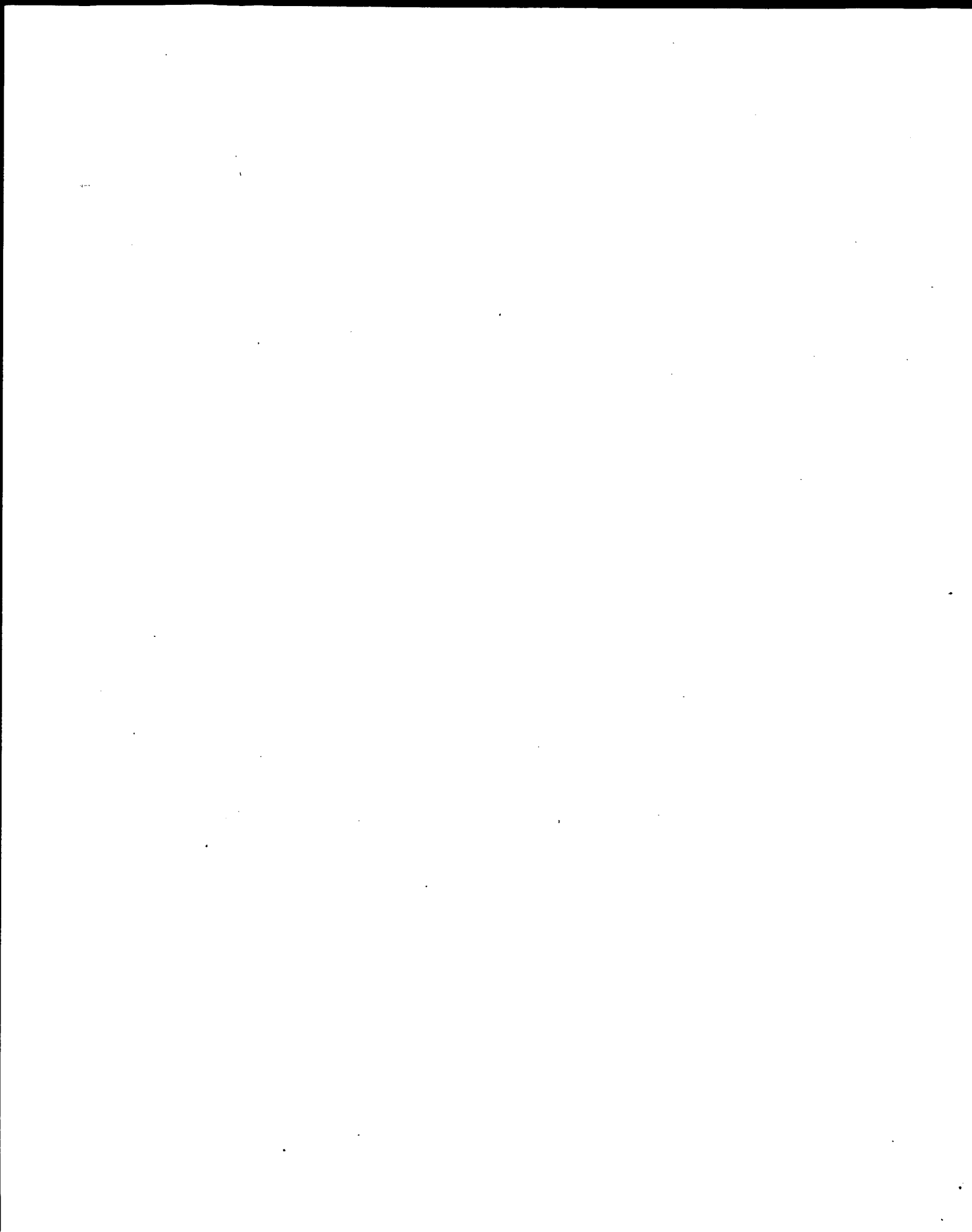
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; Sequence 3. Application US/09629430B  
; GENERAL INFORMATION:  
; APPLICANT: Hermanson, Gary George  
; TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a  
; TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer  
; FILE REFERENCE: 1530.0130001  
; CURRENT APPLICATION NUMBER: US/09/629,430B  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: 60/146,170  
; FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 7528  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; cDNA  
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Matches 1116; Conservative 0; Mismatches 295; Indels 24; Gaps 3;  
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GenCore version 5.1.6  
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Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance: to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	740.8	46.6	1676	10	US-09-815-837-82
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9	638.8	40.2	1413	9	US-10-153-382-16
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12	634.6	40.0	1428	10	US-09-740-002-17
13	630.8	39.7	1431	9	US-10-124-905-11
14	630.8	39.7	1431	9	US-09-948-429B-11
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16	626.6	39.5	1428	10	US-09-740-002-19
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18	620.2	39.1	4191	9	US-10-176-380-18
19	618.4	38.9	8120	9	US-09-726-258-68

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Sequence 571, App  
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Sequence 1604, Ap  
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25 616.8 38.8 1404 9 US-10-211-357-9  
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34 609 38.4 1392 9 US-10-153-382-4  
35 608.4 38.3 1356 10 US-09-822-698A-27  
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37 607.6 38.3 1617 10 US-09-822-830A-571  
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44 602.6 37.9 1427 12 US-10-066-895-20  
45 602.6 37.9 1427 12 US-10-066-895-25

#### ALIGNMENTS

##### RESULT 1

US-09-795-515-6  
; Sequence 6, Application US/09795515  
; Publication No. US20030039645A1  
; GENERAL INFORMATION:  
; APPLICANT: Adair, John R.  
; APPLICANT: Athwal, Diljeet S.  
; TITLE OF INVENTION: Humanised Antibodies  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/795,515  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,658  
; FILING DATE: 01-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trujillo, Doreen Yattoo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0057  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1570 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

















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RESULT 10  
US-09-859-053-31

Sequence 31, Application US/09859053

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; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
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; TYPE: DNA
; ORGANISM: Homo sapiens
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; LOCATION: (1)...(93)
; NAME/KEY: CDS
; LOCATION: (94)...(1503)
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; OTHER INFORMATION: n = A,T,C or G
; US-09-859-053-31
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Matches 1014; Conservative 0; Mismatches 474; Indels 43; Gaps 5;

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Db 116 TTTTCTGTGTGTATATAGAGGTGTCCAGTGTGAGTGTGAGTGTGAGTGTGAGG 175
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QY 115 CTGGCTAGTGTGACAGCTTCACAGAGCTGTCCATCCCTGCACAGTCTCTGTTTCTCAT 174
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Db 176 GAGGCTGTGACAGCTGGGGGTCTCTGAGACTCTCTGTCACAGCTGTGATTCACCT 235
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QY 175 TAATAGTATGTGTACACTGGGTTCCTAGTCTCCAGGAAAGGTCTGGAGTGGCTGG 234
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QY 235 GAGTATATGAGTGTGAGCAGACAGACTATATGACAGCTTTCATATCCAGACTGAGCA 294
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      ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 409 CTTATGCCATGAGTACTTGGGTCAAGGAACTCAGTCACCGTCTCTCTCAGCAAAACAA 468
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831 -----TTGTGTCGAGTGGCCACCGTGGCCAGCACC---AC 862  
826 TCGAGGTTGGACCATCCGCTTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCT 885  
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; Sequence 35, Application US/09859053  
; Patent No. US20020102658A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, No. US20020102658A1uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859,053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 1673  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)...(95)  
; NAME/KEY: CDS  
; LOCATION: (96)...(1505)  
; NAME/KEY: 3'UTR  
; LOCATION: (1509)...(1673)  
; NAME/KEY: sig\_peptide  
; LOCATION: (96)...(152)  
US-09-859-053-35

Query Match 40.0%; Score 635; DB 10; Length 1673;

Best Local Similarity 66.2%; Pred. No. 4.3e-186;  
Matches 1013; Conservative 0; Mismatches 475; Indels 43; Gaps 5;

QY 55 TCTGCTGGTGCATATCCCAAGCTGTGCTCTATCCAGGTGCAGCTGAAGCAGTCAGGAC 114  
Db 118 TTTTCTTGTTCATATATTAGAGGTGTCAGGTGTGAGGTGCAGCTGTGAGTCTGGG 177  
QY 115 CTGGCTAGTGCAGCCCTCAGAGCCTGTCCATCAGCTGCACAGTCTCTGTTCTCAT 174  
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QY 409 CTTATGCTATGAGTACTGGGTCAAGNACCTCAGTACCCTCTCCTCAGCAACAA 468  
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Db 538 AGGGCCCTTCCCTTCCCTTGGGCTCTGCTCCAGGACCTCTCCGAGACACAGCGG 597  
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449 CGTCTCTCAGCCAAACACACACACCCCATCAGTCTATCCACTGGCCCTGGGTGGAGA 508  
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429 CGTCTCTCAGTACCAAGAGGCCCATCGGTCTCCCTCCCTGGCACCCTCCCTCCCAAGAC 488  
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509 TACAACCTGTTCTCCTCGTACTCTGGGATGCTGCTCAAGGGTACTTCCCTGAGTCACT 568  
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QY 1466 ATGA 1469  
Db 1428 ATGA 1431

## RESULT 15

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; Sequence 6, Application US/10073138  
; Publication No. US20020187146A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, Darrell R.  
; HANNA, Nabil  
; BRAMS, Peter  
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING  
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7  
; AND B7.2 CO-STIMULATORY ANTIGENS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/073,138  
; FILING DATE: 13-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,361  
; FILING DATE: 08-NOV-1996  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-256  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1431 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1431  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-073-138-6

Query Match 39.6%; Score 629.2; DB 9; Length 1431;  
Best Local Similarity 67.5%; Pred. No. 2.5e-184;  
Matches 975; Conservative 0; Mismatches 433; Indels 36; Gaps 5;

QY 41 CTTGGGGTGTCTTCTGCTGGTGCACATCCAGCTGTGCTCTATCCAGGTGCAGCT 100  
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Db 69 GCAGGAGTGGGGCCCGCAGGACTGGTGAAGCTTCGGAGACCCCTGTCCCTCACCCTGGCTGT 128  
QY 161 CTCTGTTTCTCATTA---CTAGCTATGTTGATACACTGGTTCGTGCTCAGTCCAGGAAA 217  
Db 129 CTCTGGTCTCATCAGCGGTGGTATGCTGGGCTGGATCCGCCAGCCGCCAGGGAA 188





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CM nucleic - nucleic search, using sw model  
Run on: June 23, 2003, 20:18:11 ; Search time 84.1325 seconds  
(without alignments)  
5788.524 Million cell updates/sec

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Perfect score: 1588  
Sequence: 1 ccatctctctctcatagc.....taaaaaaaaaaaaaaaaaaaaa 1588  
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Gapop 10.0 , Gapext 1.0  
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Total number of hits satisfying chosen parameters: 882724

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Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/ina/PCFUS-COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	939.2	59.1	1570	2	US-08-303-569B-6
3	720.4	45.4	1572	1	US-08-353-400-23
4	674.4	42.5	1347	6	5455030-2
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6	651.2	41.0	1418	4	US-08-793-450-7
7	637.4	40.1	1418	1	US-08-467-420A-49
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14	634.6	40.0	1428	2	US-08-634-223-17
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17	634.6	40.0	1428	2	US-08-635-878-17
18	634.6	40.0	1428	2	US-08-770-057-17
19	634.6	40.0	1428	4	US-09-335-697B-17
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21	630.8	39.7	1431	3	US-08-487-550-11
22	627	39.5	1576	1	US-08-157-101A-6
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28	626.6	39.5	1428	2	US-08-770-057-19	Sequence 19, Appl
29	626.6	39.5	1428	4	US-09-335-697B-19	Sequence 19, Appl
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31	625.6	39.4	1797	1	US-08-442-542-17	Sequence 17, Appl
32	625.6	39.4	1797	3	US-08-765-469-17	Sequence 17, Appl
33	618.4	38.9	8120	3	US-09-027-449-68	Sequence 68, Appl
34	618.4	38.9	8120	3	US-09-026-985-68	Sequence 68, Appl
35	618.4	38.9	8120	4	US-09-121-952A-68	Sequence 68, Appl
36	618.4	38.9	8120	4	US-09-234-340A-68	Sequence 68, Appl
37	618	38.9	1431	3	US-08-487-550-3	Sequence 3, Appl
38	616.8	38.8	1404	3	US-08-523-894-9	Sequence 9, Appl
39	616.8	38.8	1404	3	US-08-523-894-11	Sequence 11, Appl
40	615.2	38.7	1404	3	US-08-523-894-7	Sequence 7, Appl
41	612.4	38.6	6557	1	US-08-286-740-3	Sequence 3, Appl
42	612.4	38.6	6557	5	PCN-US95-09576-3	Sequence 3, Appl
43	612.2	38.6	1350	1	US-08-157-101A-9	Sequence 9, Appl
44	603.4	38.0	1617	2	US-08-378-939-9	Sequence 9, Appl
45	598.2	37.7	1655	3	US-09-049-672A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1  
US-08-116-247-6  
; Sequence 6, Application US/08116247  
; Patent No. 5929212  
; GENERAL INFORMATION:  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Zivin, Robert A.  
; APPLICANT: Adair, John R.  
; APPLICANT: Achwal, Diljeet S.  
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,247  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/743,377  
; FILING DATE: 10-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paintin, Francis A.  
; REGISTRATION NUMBER: 19,386  
; REFERENCE/DOCKET NUMBER: CARP-0011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1570 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 41..1444  
; US-08-116-247-6

Query Match: 59.2%; Score 940.8; DB 2; Length 1570;  
Best Local Similarity 77.2%; Pred. No. 3.2e-265;

Matches 1210; Conservative 0; Mismatches 322; Indels 36; Gaps 4;  
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149 GTGAAGATGCTCTGCAAGGCTCTGGCTTACACCTTTACTAGGTACACGATGCACCTGGGTA 208  
201 CGTCAGTCTCCAGGAAGGCTCTGGAGTGGCTGGGA---GTGATATGAGTGGTGAGAC 257  
209 AAACAGAGGCTGGACAGGCTCTGGAATGGATGGATACATTAATCTAGCCGTGGTTAT 268  
258 ACAGACTAATATGAGCTTTTCATATCCAGACTGAGCATCAGCAAGGACAAATCCCAAGAGC 317  
269 ACTAATTAACAATCAGAGTTCAGAGCAAGGCCACATTCAGTACAGACAATCTCTCAGC 328  
318 CAACCTCTCTTTAAATGAACAGTCTGAGGCTACTGACAGCCATATATTAATCTGTGCC 377  
329 ACAGCTACATGCACACTGAGCAGCTGACATCTGAGGACTCTGAGTCTATTAATCTGTGCA 388  
378 AGAATAGAGGGGATATTAATATGATTTCACTATGATGCTATGAGGACTGAGGCTGAGGCA 437  
389 AGA-----TATATGATGATCATTAATCTAGCTGCTGCTGACTGAGTGGGCAAGGC 433  
438 ACCTCAGTCAAGCTCTCTCAGCAGCAACACACACCCCATCAGTCTATCCAGTGCCTCT 497  
434 ACCACTCTCAGAGTCTCTCAGCAGCAACACACAGCCCATCGTCTATCCAGTGCCTCT 493  
498 GGGTGGGAGATACAACCTGGTCTCCCTGAGTCTGGGATGCTGAGTGGTCAAGGGCTACTTC 557  
494 GTGTGGGAGATACAACCTGGTCTCCCTGAGTCTAGGATGCTGCTGCTCAAGGGTTATTTC 553  
558 CCGTGTGAGTCAAGTCAAGCTGAGTGGAACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 617  
554 CCGTGTGAGTCAAGTCAAGCTGAGTGGAACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 613  
618 CCAGTCTCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 677  
614 CCAGTCTCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 673  
678 ACCTGGCAAGTCAAGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 737  
674 ACCTGGCCAGGAGTCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 733  
738 GACAAAAAATTTGAGCCAGGGGGCCCAATTTCAACAATCAACCCCTGCTCTCCATGCAAG 797  
734 GACAGAAAAATTTGAGCCAGGGGGCC-----ACAATCAAGCCCTGCTCTCCATG---- 783  
798 GAGTCTCAAAATGCCCCAGCTCTCAACCTCGAGGAGTGGACCATCCGCTCTTCACTTCCTCT 857  
784 -----CAATGCCCCAGCACCTCAACCTCTTGGGTGGACCATCCGCTCTTCACTTCCTCT 835  
858 CCAATATCAAGGATGATCTATGATCTCCCTGACACCAAGGCTCAGTGTGTGGTGTG 917  
836 CCAAGATCAAGGATGATCTATGATCTCCCTGAGCCCATATGATCAGTGTGTGGTGTG 895  
918 GATGTGAGGAGGATGATCTCAAGCTCTCAGATCAGTGTGTGTGTAACAACCTGGAAGTA 977  
896 GATGTGAGGAGGATGATCTCAAGCTCTCAGATCAGTGTGTGTGTAACAACCTGGAAGTA 955  
978 CACAGCTCTCACACACAAACCATAGAGAGGATTAACAACGATCTATCCGGGTGTGTCAGC 1037  
956 CACAGCTCTCACACACAAACCATAGAGAGGATTAACAACGATCTATCCGGGTGTGTCAGT 1015  
1038 ACCCTTCCCCATCCAGCACCAGGAGTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1097  
1016 GCGCTTCCCCATCCAGCACCAGGAGTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1075

QY 1098 AACAAAGACCTCCCATCACCATCCAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGA 1157  
Db 1076 AACAAAGACCTCCAGCGCCATCCAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGA 1135  
QY 1158 GCTCCACAAGTATACATCTTCCGCCACACAGAGAGTGTCTCCAGGAAAGATGTCAGT 1217  
Db 1136 GCTCCACAAGTATATGCTTCCCTCCACCAAGAGAGATGACTTAAGAAACAGGTCACT 1195  
QY 1218 CTCATCTCCCTGGTCTGAGGCTTCAACCTCCAGAGATCAGTGTGGAGTGGACCAAGCAAT 1277  
Db 1196 CTGACCTGCATGGTCAAGACTTCTATGCTGAGACATTTACGTGGAGTGGACCAAGCAAC 1255  
QY 1278 GGGATACAGAGGAGAACTACAAGGACACCCGACAGCTCTGAGTCTGAGGTTCTTTAC 1337  
Db 1256 GGGAAACAGAGCTAAACTACAAGAAACACTGAACCACTCTGAGTCTGATGGTCTTTAC 1315  
QY 1338 TTCATATATAGCAAGCTCAATATGAAACACAGCAAGTGGGAGAAACAGATTCCTTCTCA 1397  
Db 1316 TTCATGTACAGCAAGCTCAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCC 1375  
QY 1398 TGCACAGTGCAGACAGGAGGCTGTGAATAATTAACCTGAAGAAGACCATCTCCCGGCT 1457  
Db 1376 TGTTCAGTGGTCCAGGAGGCTGTGCACAATCACCACAGACTTAAGAGCTTCTCCCGGACT 1435  
QY 1458 CCGGTAATGAGCTCAGCAGCCACAAAGCTCTCAGGCTCTAAGAGAGACTGGACCCCAT 1517  
Db 1436 CCGGTAATGAGCTCAGCAGCCACAAAGCTCTCAGGCTCTAAGAGAGACTGGACCCCAT 1495  
QY 1518 ATCCATGATCCCTGTATATAAAGCATCAGCAAGCTGGTGGTGGTGGTGGTGGTGGTGGT 1577  
Db 1496 CTCCATGCTTCCCTGTATATAAAGCAACCCAGCAATGCTGGGACCATGTAAAAAAA 1555  
QY 1578 AAAAAAA 1585  
Db 1556 AAAAAAA 1563

## RESULT 2

US-08-303-569B-6  
; Sequence 6, Application US/08303569B  
; Patent No. 5859205  
; GENERAL INFORMATION:  
; APPLICANT: Adair, John R.  
; APPLICANT: Athwal, Diljeet S.  
; APPLICANT: Emtage, John S.  
; TITLE OF INVENTION: Humanised Antibodies  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/303,569B  
; FILING DATE: 07-SEP-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trujillo, Doreen Yanko  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:











REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1418 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1418  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1..57  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 58..1418  
OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY  
OTHER INFORMATION: CHAIN"  
US-08-793-450-7

Query Match 41.0%; Score 651.2; DB 4; Length 1418;  
Best Local Similarity 67.5%; Pred. No. 1.4e-180;  
Matches 958; Conservative 0; Mismatches 438; Indels 24; Gaps 2;  
52 TCCTCTGCTGGTACATTCCTCAAGCTGTCTTCCAGCTGAGCTGAAGCTGAG 111  
112 GACCTGGCTAGTGCAGCCCTCACAGAGCTCTCCATCACCTGCACAGTCTCTGTTTCT 171  
80 GCGCAGGACTGTGAAGCTTCGGAGACCTCTGCTCCCTCACCTGCAGTCTATGTTGGT 139  
172 CATTAACCTAGCTATGGTGTACACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 231  
140 CTTTCAGTGGTGTACTGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199  
232 TGGGAGTGTATGGAGTGTGGAGACAGACTATAATGCAGCTTTCATATCCAGACTGA 291  
200 TGGGGAATCAATCATAGTGAAGACCAACTACAAACCTGCTCCAGAGTCAAGTCA 259  
292 GCATCAGCAAGGACAAATTCAGAGACCAACTCTCTTTAAATGAACAGTCTGCGAGCTA 351  
260 CCATATCAGTACAGACCTCCAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319  
352 CTGACACAGCCATATATTAATCTGTGCGAGAAATAGAGGGGATATTTACTATGATTTT 411  
320 CGGACACGGCTGTGTATTAATCTGTGCGAGGGCCAGAGTATAAATGGAAGTATCATGG 379  
412 ATGCCATGGACTAGTGGGTGAAGAACTCAGTCAACCTGCTCCCTGCTCCCTGCTGCTC 471  
380 ACTGGTTCAGCCCTGGGGGCAAGTACCACTGTCAACCTGCTCCCTGCTCCCTGCTC 439  
472 CCCCATCAGTCTATCCATGCGCCCTGGGTGGAGATACAACTGTTCTCCCTGCTGCTC 531  
440 GCGCATCGCTCTTCCCTGCGACCTCTCTCAAGAGCACTCTGCGGGGACAGCGGGCC 499  
532 TGGGATGCTGTGTAAGGGCTACTTCCCTGAGTCACTGCTGCTGCTGCTGCTGCTGCTG 591  
500 TGGGCTGCTGTGTAAGGACTACTTCCCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 559  
592 CCCTGCTCAGCAGTGTGACACCTTCCAGCTCTCTCTGAG---TCTGGACTCTACACTA 648  
560 CCTGACAGCGGGCTGACACCTTCCCGGCTGCTCTACAGTCTCAGACTCTACTCTCC 619  
649 TGAGCAGCTCAGTGTGCTGCTCCCTCCAGCCTGCGCAAGTCAAGCTGCTCAGCTGCG 708  
620 TCAGCAGCGGTGTGACCTGCTCCAGCAGCTTGGGACCCAGACCTACATCTCAACG 679  
709 TTGCTCACCACCCAGCAGCAGCAGCTGGTGGACAAAACCTTGAGCCCGGCGCCATT 768

## RESULT 7

US-08-467-420A-49  
; Sequence 49, Application US/08467420A  
; Patent No. 5683892  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; CORRESPONDENCE ADDRESSES: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 74  
; ADDRESS: SmithKline Beecham Corp./Corporate  
; ADDRESS: Intellectual Property  
; STREET: P. O. Box 1539-UM2220  
; CITY: King of Prussia

680 TGAATCACAGCCAGCACACCAAGTGGACAAAGAGCAGAGCC----- 725  
769 CAACAATCAACCCCTGTCTCCATGCAAGAGTGTTCACAAATCCAGCTCTCTTAACCTCG 828  
726 -----CAAACTCTGTGACAAAACCTCAGACATGCCACCGTCCCGCAGACCTGAACCTC 778  
829 AGGGTGGACCATCCGCTCTTCATCTTCCCTCCAATATCAAGGATGTACTCATGATCTCC 888  
779 TGGGGGAGCGGTGAGTCTTCTCTTCCCGCCAAAACCAAGGACACCTCATGATCTCC 838  
889 TGACACCCCAAGGTCACTGT 948  
839 GGACCCCTGAGGTCACTGT 898  
949 TCAGCTGGTGTGTGAACAACGTGAAAGTACACACAGCTCAGACACAAACCCATAGAGAG 1008  
899 TCACCTGGT 958  
1009 ATTACACAGTACTATCCCGGGT 1068  
959 AGTACAACAGCACTTACCGGGT 1018  
1069 GTGGCAAGGAGTCAAAATGCAAGGTCAACAACAAAGACCTCCCATCACCATCGAGAGAA 1128  
1019 ATGGCAAGGAGTCAAAATGCAAGGTGTCCAACAAGCCCTCCCGAGCCCATTTGAGAAA 1078  
1129 CCATCTCAAAAATTAAGGGT 1188  
1079 CCATCTCAAAAATTAAGGGT 1138  
1189 CAGAGCAGT 1248  
1139 GGGATGAGT 1198  
1249 GAGACATAGT 1308  
1199 GGGACATCGCTGT 1258  
1309 CACCATGCTGT 1368  
1259 CTTCCGT 1318  
1369 GCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGTGTGTGTGTGTGTGTGTGTGTGT 1428  
1319 GCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1378  
1429 ACTACTGAAAGAGCACTCTCCCGGTCTCCCGGTAAATG 1468  
1379 ACTACAGCAGAGAGAGGCTCTCCCTGTCTCCGGTAAATG 1418









2357 ATGCATGAGGCTGTCACAACTACACGAGAGAGCCTCTCCCTGCTCCTCGGTAAG 2416  
1467 TGAGCTAG 1475  
2417 TGAGTGTAG 2425

RESULT 10  
JS-08-940-371-49  
Sequence 49, Application US/08940371  
Patent No. 5851525  
GENERAL INFORMATION:  
APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TREATMENT OF IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P. O. Box 1539-0W2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,371  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,110  
FILING DATE:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50282  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610 270-5024  
TELEFAX: 610 270-5090  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
S-08-940-371-49

Query Match 40.1%; Score 637.4; DB 2; Length 6285;  
Best Local Similarity 68.2%; Pred. No. 3.3e-176;  
Matches 947; Conservative 0; Mismatches 406; Indels 36; Gaps 3;

90 CAGGTGCGCTGAGCAGTACGAGACCTGGCCTAGTCAGAGCCCTCAGAGCCCTGTCCATC 149  
1070 CAGGTTACCTCGGTGAATCCGCTCGGCACTAGTTAAACCCGACCCAGACCCCTGACGTTA 1129  
150 ACCTGCACAGTCTCTGTTCTCATTAACCTAGCTATGGTGTACACTGGGTTCTGTCAGTCT 209  
1130 ACCTGCACCGTCTCCGGTTCTCCCTGACGAGCTAGTGTACACTGGGTTCCGCTCAGCCG 1189

QY 210 CCAGAAAGGGTCTGAGTGGCTGGAGTGATATGAGTGGTGGAGACACACACTATAAT 269  
Db 1190 CCGGTAAGGTTCTAGATGGCTGGTGTAAATATGGCTAGTGGAGGACAGATTATAAT 1249  
QY 270 GCAGCTTTCATATCCAGACTGAGCAATTCACAGGACAATTCACAGCAACTCTCTTT 329  
Db 1250 TCGGCTCTCATGTCCTGCTGTCGATATCCAAAGACACCTCCCGTAACAGGTTGTTCTG 1309  
QY 330 AAAATGAACAGTCTCGGAGCTACTGACACAGCAGCATATATGCTGCCAGAAATAGAGG 389  
Db 1310 ACCATGACTAATGACCGGTTGACACCGCTACTCTACTGCTGCTGCGTACG 1362  
QY 390 GATATTTACTATGATTTCATTTATGCCATGAGTACTGGGGTCAAGGAACCTCAGTACC 449  
Db 1363 -----TCGCCCTTCTTCTTACTACGGCTTACTAGGGTCTGGTACCCAGCTTACC 1417  
QY 450 GTCCTCTCAGCAAAACACACACCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAGAT 509  
Db 1418 GTGAGCTCAGCTAGTACCAGGGCCCATCGGCTTCCGCCCTGGCACCTCTCCCAAGAGC 1477  
QY 510 ACACTGGTCTCTCGTACTGCTGGGATGCTTCAAGGGCTACTTCCCTGAGTCAGT 569  
Db 1478 ACCTCTGGGGCAGACGCGCTGGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1537  
QY 570 ACTGTGACTTGAACCTCTGGATCCCTGTCAGCAGTGTGCACACCTTCCAGCTCTCTG 629  
Db 1538 ACGGTGCTGGAACCTCAGCGCCCTGACAGGCGCTGCACACCTTCCGCTGCTCTA 1597  
QY 630 CAG---TCTGGACTCTACACTATGAGCAGTCTGAGTGTGCTCCCTCAGCAGCTGGCA 686  
Db 1598 CAGTCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGC 1657  
QY 687 AGTCAGCCGTCACCTGACGAGTGTCTCACCAGCAGCAGCAGCAGCAGTGGACAAAAA 746  
Db 1658 ACCAGACCTTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGACAGAGA 1717  
QY 747 CTTGAGCCAGCGGCGCCATTTCAACAATCAACCCCTGCTCTCCATGCAAGGAGTGTAC 806  
Db 1718 GTTGAGCC-----CAATCTTGTGACAAACTCAGACTGCCA 1756  
QY 807 AAATGCCAGCTCTTAACCTCGAGGTTGGACCATTCCTTCTCATCTTCCCTCCAAATATC 866  
Db 1757 CCGTGGCCAGCACCTGAACCTCTGGGGGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCT 1816  
QY 867 AAGGATGTACTATGATCTCTCTGACACCCAGGTGAGTGTGCTGCTGCTGCTGCTGCTG 926  
Db 1817 AAGGACACCTCTATGATCTCTCGGACCTCTGAGGTACATGCTGCTGCTGCTGCTGCTG 1876  
QY 927 GAGGATGACCCAGAGTCCAGATCAGTGTGTTGTGAACAAGTGGAGTACACACACT 986  
Db 1877 CACGAAGACCTCGAGTCAAGTTCAACTGCTGACGCGCTGAGGAGTGGAGTGCATATGCC 1936  
QY 987 CAGACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGTGGTGGAGTGGAGTGG 1046  
Db 1937 AAGACAAAGCCCGGAGGAGCAGTACACAGCAGTACCTGCTGGTGGTGGTGGTGGTGG 1996  
QY 1047 ATCCAGCAGCAGGAGTGGATGAGTGGCAAGGTTCAAAATCAAGGTCAACAAACAGAC 1106  
Db 1997 GTCTGACAGGAGTGGCTGAATGGCAAGGAGTACAGTCAAGGTCTCAACAAAGCC 2056  
QY 1107 CTCCATCACCCATCGAGAGAACCATCTCAAAATTTAAAGGGCTAGTCAGAGCTCCACAA 1166  
Db 2057 CTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGAGGAGGAGGAGGAGGAGGAG 2116  
QY 1167 GTATACATCTTGGCGCCAGCAGCAGTGTGCTCAGGAAAGATGTGCTGCTGCTGCTGCT 1226  
Db 2117 GTGTACACCTTGGCGCCATCCCGGAGGAGATGACCAAGAACAGGTGCTGCTGCTGCTG 2176  
QY 1227 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1286  
Db 2177 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2236



2117 GTGTACACCTGCCCTCCATCCCGGAGGAGATGACCAAGAACCCAGGTGACCTGC 2176  
1227 CTGTCGTGGGCTCAACCTCGGACACATCAGTGGAGTGACACCAATGGGCATACA 1286  
2177 CTGGTCAAGGCTTCTATCCGACGACATCGCGTGGAGTGGAGCAATGGGACCG 2236  
1287 GAGGAGAACTACAAGGACACCGCACCTCTGAGTCTGAGGTTCTTACTTCATATAT 1346  
2237 GAGAACACTACAGACACCGCTCCGCTGGTGGACTCGGACGGTCTCTTCTCTAT 2296  
1347 AGCAAGCTCAATATGAAACCAAGCAAGTGGGAGGAAACAGATTCCTTCTCATGCAACGTG 1406  
2297 AGCAAGCTCAAGTGGGACAGAGAGAGTGGGAGGAGGGAACGTCTTCTCATGCTCCGTG 2356  
1407 AGACACGAGGCTCGAAAATTAATCTACCTGAAGAGACATCTCCCGTGGCGGTAATA 1466  
2357 ATGATGAGGCTCTGCACAACCACTACACGAGAGAGGCTCTCCCTCTCCGGGTAAG 2416  
1467 TGAGCTCAG 1475  
2417 TGAGTGTAG 2425

## RESULT 12

PCT-US95-17082A-49

Sequence 49, Application PC/TUS9517082A

## GENERAL INFORMATION:

APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TREATMENT OF IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 76

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: Smithline Beecham Corp./Corporate  
STREET: P.O. Box 1539-UW2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17082A  
FILING DATE:

## CLASSIFICATION:

Prior Application Data:

Application Number: US 08/470110

Filing Date: 06-JUN-1995

## Prior Application Data:

Application Number: US 08/467420

Filing Date: 06-JUN-1995

## Prior Application Data:

Application Number: US 08/363131

Filing Date: 23-DEC-1994

## Attorney/Agent Information:

Name: Sutton, Jeffrey A.

Registration Number: 34, 028

Reference/Docket Number: P50282-2

Telecommunication Information:

Telephone: 610-270-5024

Telefax: 610-270-5090

Information for Seq ID No: 49:

## Sequence Characteristics:

LENGTH: 6285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
PCT-US95-17082A-49

Query Match 40.1%; Score 637.4; DB 5; Length 6285;  
Best Local Similarity 68.2%; Pred. No. 3.e-176;  
Matches 947; Conservative 0; Mismatches 406; Indels 36; Gaps 3;

QY 90 CAGGTGTCAGCTCAAGCAGTCAGGACCTGGCCCTAGTGTGACGCCCTCACAGAGCGTGTCCATC 149  
Db 1070 CAGGTACCTCCGTCGATCCCGTCGGCAGCACTAGTTAAACCCAGCCCTGACGTTA 1129  
QY 150 ACCTGCACAGTCTCTGGTTTCTATTAAGTATGTTGTACACTGGTGTGGTCTGCTAGTCT 209  
Db 1130 ACCTGCACCGTCTCCGGTTTCTCCCTGACGAGTATAGTGTACACTGGTGTGGTCTGAGCG 1189  
QY 210 CCAGGAAGGGTCTGGAGTGGCTGGGAGTGATATGAGTGGTGGAGACACAGACTATAAT 269  
Db 1190 CCGGGTAAAGGTCTAGAAATGGCTGTAATATGGCTAGTGGAGGCACAGATTATAAT 1249  
QY 270 GCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAAATTCAGAGGCCAATCTCTCTT 329  
Db 1250 TCGGCTCTCATGTCCCGTCTGTGATATCCAAAGACACCTCCCGTAACAGGTTGTTCTG 1309  
QY 330 AAATGAACAGTCTCGAGTACTGACACAGCATATATTAAGTGTGCCAGAAATAGAGGG 389  
Db 1310 ACCATGACTAATGAGACCGGTTGACACCGTACTACTGCTGCGCTCGAGA----- 1362  
QY 390 GATATTACTATGATTTCACCTTATGTCATGCTGGGTCAAGAGGACCTCAGTCACT 449  
Db 1363 -----TCCCGCTTCTTCTTACTAGCGCTTGTACTGGGTGCTGGTACCCAGTTACC 1417  
QY 450 GTCTCCTCAGCCAAACAAACACCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAGAT 509  
Db 1418 GTAGCTCAGCTAGTAGTACCAAGGGCCCATCGGCTTCTCCCGTGGCACCTCTCCCAAGAGC 1477  
QY 510 ACAACTGGTCTCTCGTACCTGCTGGATGCTGGTCAAGGGGCTACTTCCCTGAGTCAGTG 569  
Db 1478 ACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGCAACCGGTG 1537  
QY 570 ACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCCCTG 629  
Db 1538 ACGTGTCTGTGGAATCAGGCGCCCTGACCGGGGTGCACACCTTCCCGCTGTCTTA 1597  
QY 630 CAG---TCTGGACTCTACACTATGACAGCTCAGTCACTGTCCCTCCAGCACCTGGCCA 686  
Db 1598 CAGTCTCAGGACTCTACTCCCTCAGAGCGTGTGACCGTCCCTCCAGCAGCTTGGC 1657  
QY 687 AGTCAGCCGTCACCTGACGGTTGCTCACCCAGCAGCAGCAGCAGCGTGGACAAAAA 746  
Db 1658 ACCCAGACCTACATCTGCAAGTGAATCAAGCCAGCAACACCAAGTGGACAAGAGA 1717  
QY 747 CTTGAGCCCGAGGGGCCCATTTCAACATCAACCCCTGTCTCCATGCAAGGAGTGTAC 806  
Db 1718 GTTGAGCC-----CAATCTTGTGACAAACATCACAATGCGCCA 1756  
QY 807 AAATGCCCGAGCTCCTAACTCGAGGTTGGACCATCCGCTTTCATCTTCCCTCAAAATATC 866  
Db 1757 CCGTCCCGCAGCACCTGAACTCTGGGGGACCGCTCAGTCTTCTTCTTCCCGCAAAACCC 1816  
QY 867 AAGGATGTACTCATGATCTCCCTGACACCCCAAGTCACTGTGGTGGTGGTGGTGGAGC 926  
Db 1817 AAGCACCCCTCATGATCTCCCGGACCCCTCAGGTACATGCGTGGTGGTGGTGGAGC 1876  
QY 927 GAGGATGACCCAGACGTCAGATCAGTGGTTTGTGAACACGTTGGAAGTACACACAGCT 986  
Db 1877 CACGAAGACCCCTGAGTCAAGTTCAGTGGTACGTCGCGGCGGTGGAGTGCATATGCC 1936  
QY 987 CAGACAAACCCATAGAGGATTACACAGTACTATCCGGGTGGTGGAGCAGCTCCCTCC 1046  
Db 1046 CAGACAAACCCATAGAGGATTACACAGTACTATCCGGGTGGTGGAGCAGCTCCCTCC



842 TCTCCGCGACCTGAGTGCATCGTGGTGGACGTGAGCCACGAGACCTTGAGG 901  
943 TCCACATCAGCTGTTGTGAACAGCTGGAAGTACACACGCTCAGACACAAACCCATA 1002  
902 TCAAGTCACTGAGTGGTGGACGCGGTGGAGGTGCATTAATGCCAAGACAAAGCGCGGG 961  
1003 GAGAGGATTACACAGTACTATCCCGGGTGGTGGACGACCTCCCGCATCCAGCAGGAGCT 1062  
962 AGGACGAGTACACAGCAGTACCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1021  
1063 GGATGAGTGGCAGGAGTGAATGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGA 1122  
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1382 ACACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1428

RESULT 14  
JS-08-634-223-17  
Sequence 17, Application US/08634223  
Patent No. 5840298  
GENERAL INFORMATION:  
APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Soulaïma Salim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.  
APPLICANT: HEARD, Cheryl Janne  
APPLICANT: NEWMAN, Roland Anthony  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,223  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,376

FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1428 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1428  
US-08-634-223-17  
Query Match 40.0%; Score 634.6; DB 2; Length 1428;  
Best Local Similarity 67.6%; Pred. No. 1e-175;  
Matches 965; Conservative 0; Mismatches 429; Indels 33; Gaps 4;  
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1423 AAATTTACTACTCTGAAGAGACCATCTCCCGTCTCCGGGTAAATGA 1469  
1382 ACAACCATACACGAGAGAGCGCTCTCCCTGCTCTCCGGGTAAATGA 1428

3-08-634-224-17  
Sequence 17, Application US/08634224  
Patent No. 5866125  
GENERAL INFORMATION:  
APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Soulaina Selim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.  
APPLICANT: HEARD, Cheryl Janne  
APPLICANT: NEWMAN, Roland Anthony  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,224  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/488,376  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1428 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
NAME/KEY: CDS  
LOCATION: 1..1428  
US-08-634-224-17

Query Match 40.0%; Score 634.6; DB 2; Length 1428;  
Best Local Similarity 67.6%; Pred. No. 175;  
Matches 965; Conservative 0; Mismatches 429; Indels 33; Gaps 4;  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

June 23, 2003, 16:23:42 ; Search time 397.773 Seconds  
(without alignments)

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
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	2	1081.2	68.1	1365	24	ABU56966	Recombinant 4G10 a
	3	963	60.6	1645	15	AAQ54652	T84.12 Heavy chain
	4	940.8	59.2	1570	12	AAQ12837	Monoclonal antibody
	5	933	58.8	1581	14	AAQ48037	Monoclonal antibody
	6	885	55.7	7528	22	AAF30316	Bicistronic idioty
	7	801.8	50.5	1341	10	AAW91659	Chimeric antibody
	8	768.2	48.4	1431	22	AAQ91017	Chimeric 4H6 anti-
	9	768.2	48.4	1431	22	AAQ91018	Chimeric 4H6 anti-

10	740.8	46.6	1676	23	ABI99041	Murine pCB223 codi
11	737.8	46.5	1679	22	AAF30341	Bicistronic heavy cha
12	720.4	45.4	1582	16	AAQ94037	MAB 55.1 heavy cha
13	716.8	45.1	1528	5	AA40015	mRNA encoding gamm
14	713.6	44.9	1528	5	AA40015	Combined cDNA inse
15	690.6	43.5	1553	16	AAQ79930	Anti-tobacco mosai
16	685.6	43.2	1347	17	AAQ51534	Sequence encoding
17	685.6	43.2	1347	17	AAQ51534	Murine anti-BGH MA
18	684.8	43.1	2053	23	ABI99029	IAS MBP 90-101 CH1
19	684.8	43.1	2059	23	ABI99032	MBP 1-14 CH1.H.CH2
20	683.6	43.0	1347	11	AAQ05708	Heavy chain of ant
21	680.8	42.9	1347	11	AAQ13733	Anti-bGH monoclon
22	670.6	42.2	1398	24	AAQ97062	DNA encoding TRA-8
23	662	41.7	1516	24	AAQ29308	Human penton base
24	656.8	41.4	1634	21	AAZ50012	Human immune syste
25	654.6	41.2	1798	21	AAQ98320	Human colon cancer
26	651.8	41.0	1567	22	AAQ66522	Human immune syste
27	651.2	41.0	1418	17	AAQ26889	Anti-rhesus D reco
28	648.8	40.9	1392	19	AAV70129	Anti-Fas MAb HFE7A
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30	648.8	40.9	1392	21	AAAL1546	Murine anti-Fas an
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33	647.6	40.8	1431	17	AAQ18059	Monoclonal antiob
34	643.6	40.5	1644	22	AAQ22593	Human cDNA encodin
35	638.8	40.2	1413	21	AAA46898	DNA encoding the h
36	638.6	40.2	1430	24	AAQ98701	cDNA of the heavy
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39	636.2	40.1	1428	18	AAQ61241	Human anti-RSV mon
40	635.8	40.0	6285	17	AAQ34109	Anti-IL-5 humanise
41	635.4	40.0	1386	14	AAQ53429	Sequence encoding
42	635	40.0	1673	24	AAQ59476	Anti-human AILIM m
43	630.8	39.7	1431	18	AAQ62513	Primate anti-hu
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## ALIGNMENTS

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AC	ABL56968;
XX	
DT	15-JUL-2002 (first entry)
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DE	Recombinant 4G10 antibody heavy chain-6His coding sequence.
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KW	Monoclonal antibody; antibody; 4G10; phosphotyrosine; cancer;
KW	diagnosis; gene; ss.
XX	
OS	Unidentified.
OS	Synthetic.
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FT	/*tag= a
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PN	WO200218443-A2.
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XX	07-MAR-2002.
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PF	30-AUG-2001; 2001WO-US26926.
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PPR	01-SEP-2000; 2000US-0653755.
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PPA	(UPST-) UPSTATE BIOTECHNOLOGY INC.



















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RESULT 9

AAC91018/C

ID AAC91018 standard; DNA; 1431 BP.

XX AAC91018;

AC

DT 15-MAR-2001 (first entry)

XX Chimeric 4H6 anti-DR4 antibody heavy chain complementary DNA.

DE Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;

KW autoimmune; ds.

KX Homo sapiens.

OS Synthetic.

OS

PN WO200073349-A1.

XX

PD 07-DEC-2000.

PF 25-MAY-2000; 2000WO-US14599.

XX

PR 28-MAY-1999; 99US-0322875.

XX (GETH ) GENENTECH INC.

PA Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;

PI WPI; 2001-041145/05.

XX

DR Novel anti-death receptor 4 antibodies useful for treating cancer and

PT immune related disorders such as rheumatoid arthritis, sjogren's

PT syndrome, Grave's disease and diabetes mellitus -

XX Disclosure; Fig 18; 126pp; English.

XX The present invention relates to an anti-Death receptor 4 (DR4)

CC antibody. The antibodies of the invention are useful for inducing

CC apoptosis in mammalian cancer cells such as colon cancer cells and

CC for treating an immune-related disease in a mammal such as arthritis

CC and autoimmune disease.

SX

SQ Sequence 1431 BP; 273 A; 367 C; 438 G; 350 T; 3 other;

Query Match 48.4%; Score 768.2; DB 22; Length 1431;

Best Local Similarity 72.8%; Pred. No. 1e-178;

Matches 1043; Conservative 3; Mismatches 351; Indels 36; Gaps 3;

QY 52 TCTTCTGCTGCTGATCCCAAGCTGTGCTTATCCAGTGTGAGTGAAGCAGTCA 111

DB 1412 TCTTTTCTAGTACCACTGCAACTGGAGTACATTCASARGTKCAGCTGAAGAGTCA 1353

QY 112 GACCTGGCTAGTGCAGCCCTCAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTCT 171

DB 1352 GACCTGGCTGGTGGCGCCCTCAGAGCCTGTCCATCACTTGCACGTGCTCTGGGTTT 1293

QY 172 CATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGCTCTGGAGTGC 231

Db 1292 CATTAACAGCTATGGGTACACTGGGTTGCCAGCCTCCAGAAAGGGCTCTGGAGTGC 1233  
QY 232 TGGGAGTATGATGGAGTGGTGAGACACAGACTATAATGACAGCTTTTCATATCCAGACTGA 291  
Db 1232 TGGGAGTATGATGGGCTGTGGAACACAAATATATTCGGCTCTCATGTCCAGACTGA 1173  
QY 292 GCATCAGCAAGAGCAAAATTCGAAGGCCAACTCTCTTTTAAATGAACAGTCTGCGAGCTA 351  
Db 1172 GCATCAGCAAGAGCAAACTCCAAGAGCCAAAGTTTCTTAAATGAACAGTCTGCAAACTG 1113  
QY 352 CTGACAGAGCCATATATTAATCTGTGCGCAAAATAGAGGGATATTTACTATGATTTCACT- 410  
Db 1112 ATGACAGAGCCATGTAATCTGTGCGCAAGAGGGGAATTCGATTAATCTACGCTAGTAGTC 1053  
QY 411 -----TATGCCATGGACTACTGGGTCAAGGAACCTCACTACCCGCTCTCTCAG 459  
Db 1052 TCCTATCTTACATTTCTATGAACTTCTGGGTCAAGGAACCTCACTACCCGCTCTCTCAG 993  
QY 460 CCAAAACACACCCCATCACTATCCACTGGCCCTGGGTGTGGAGATACAACTGGTT 519  
Db 992 CCAAAACAGGGCCCATCGCTCTTCCCTGGCACCTCTCCAGAGCACCTCTGGG 933  
QY 520 CCTCGTGAATCTGGGATGCTGTGCAAGGCTACTTCCCTGAGTCAGTACTGTGACTT 579  
Db 932 GCACAGCGGCTGGGCTGGTGTGCAAGGCTACTTCCCGGAACCGGTGAGGTGCTG 873  
QY 580 GGAATCTGGATCCCTGTGCAAGAGTGTGACACCTTCCAGCTCTCTGAG---TTG 636  
Db 872 GGAATCTAGGCGCCCTGACAGCGCGTGCACACCTTCCCGCTCTCTACAGTCTCTCAG 813  
QY 637 GACTCTACATATGAGCAGCTCAGTGTGCTCCCTCCAGCACCTGGCCAGTCAGACGG 696  
Db 812 GACTCTACTCCTCAGCAGCGTGTGACTGTGCTCTGAGCAGCTTGGGACCCAGAGCT 753  
QY 697 TCACCTGAGCGTGTGCTCACCGCAGCAGCAGCAGCGTGGCAAAAAAATCTGAGCCCA 756  
Db 752 ACATCTGCAAGCTGAATCACAAGCCCAACACCAAGGTGGACAAGAAAGTTGAGCC-- 695  
QY 757 GCGGCGCAATTTCAACAAATCAACCCCTCTCTCCATGCAAGAGTGTCCAAAATCCCGCAG 816  
Db 694 -----CAATCTGTGCAAAAATCAACATGCGCCACATGCGCCCGCCAG 654  
QY 817 CTCCTAACCTCGAGGTGAGCATCCGCTCTCATCTTCCCTCCAAATATCAAGATGTAC 876  
Db 653 CACCTGAACCTCTGGGGGACCGTCACTCTCTCTCCCTCCCAAAACCCCAAGACACCC 594  
QY 877 TCATGATCTCCTGACACCCAAAGTCACTGTGTGGTGTGAGTGTGAGCGAGGATGACC 936  
Db 593 TCATGATCTCCGAGCCCTGAGTCACTGCGTGTGAGTGTGAGCGTGGCCAGGAGACC 534  
QY 937 CAGAGCTCCAGATCAGCTGTGTTGTGAACAACGCTGGAAGTACACACAGCTCAGACACAAA 996  
Db 533 CTGAGGTCAAGTCAACTGGTACGTGGACGCGTGGAGTGCATTAATGCCAAGACAAAGC 474  
QY 997 CCCATAGAGAGATTACAACTACTATTCCTGGGTGTGAGCAGCCCTCCCATCCAGCACC 1056  
Db 473 CGCGGGAGGAGCAGTACAAACAGCAGTACCGGCTGCTCAGCGTCTCTCAGCTGACCC 414  
QY 1057 AGGACTGATGAGTGGCAAGAGTTCAATCCAGGTTCAACAAAGAACCTCCCATCAC 1116  
Db 413 AGGACTGCTGAATGGCAAGAGTACAGTCCAAAGTGTCCAAAGAACCCCTCCAGGCC 354  
QY 1117 CCATCGAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGCTCCCAAGTATACATCT 1176  
Db 353 CCATCGAAGAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGACCAAGGTGTACACC 294  
QY 1177 TGCGCCGACAGCAGAGCAGTGTGTCAGGAAGATGTCACTGCTGCTGCTGTGCTGG 1236  
Db 293 TGCCCCCATCCCGGAGAGATGACCAAGACCAAGTCAAGCTGACCTGCTGCTGCTCAAG 234  
QY 1237 GCTTCAACCTTGGAGACATCAGTGTGGAGTGGACCAATGGGACATACAGAGAGACT 1296  
Db 233 GCTTCTATCCAGGACATCCCGCTGGAGTGGGAGAGCAATGGGACCGGAGACACT 174

QY 1297 ACAAGGACACCCACCAGCTCTGGAGTCTGAGCGTCTTACTTATATATAGCAAGCTCA 1356  
Db 173 ACAAGGACACCGCTCCGCTGCTGGAGTCCGAGCGCTCTTCTTCTTACAGCAAGCTCA 114  
QY 1357 ATATGAAAAACAAGCAAGTGGGAGAAACAGATTCTCTCATGCAACGTGAGACAGGAG 1416  
Db 113 CCGTGACAAAGAGCAGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTCATGATGATGAGS 54  
QY 1417 GTCTGAAAAATTAATCTACCTGAGAGAGACCATCTCCCGGTCTCCGGGTAAATGA 1469  
Db 53 CTCTGCACAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1

## RESULT 10

ABI99041

ID ABI99041 standard; cDNA; 1676 BP.

XX AC ABI99041;

XX AC ABI99041;

DT 25-FEB-2002 (first entry)

XX Murine PCB223 coding sequence.

DE Mouse; MHC; major histocompatibility complex; MHC class II; multimer;

XX single chain; immunosuppressive; antidiabetic; antinflammatory;

KW antianemic; anti-rheumatoid; antiarthritic; neuroprotective; vaccine;

KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;

KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;

KW rheumatoid arthritis; systemic lupus erythematosus; ss.

XX Mus sp.

OS Synthetic.

XX WO200170245-A1.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-US09616.

XX 22-MAR-2000; 2000US-191274P.

PR 15-MAY-2000; 2000US-204249P.

PR 23-JAN-2001; 2001US-264003P.

XX (CORI-) CORIXA CORP.

XX Carter D, Zhu S, Arimilli S, Wang A;

XX WPI; 2001-616371/71.

DR P-PSDB; ABB56471.

XX Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha and beta domain linked through amino acid linker and multimerization domain

PS Disclosure; Page 115; 147pp; English.

XX The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha domain and a beta domain linked through an amino acid linker and a multimerization domain. The first and the second molecule are linked through the multimerization domain to form a multimeric complex. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (RAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention.

XX Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 other;

Query Match 46.5%; Score 740.8; DB 23; Length 1676;  
 Best Local Similarity 84.7%; Pred. No. 5.7e-172;  
 Matches 861; Conservative 0; Mismatches 137; Indels 18; Gaps 2;

456 TCAGCCAAACAAACACCCCTAGTCTATCCACTGGCCCTGGTGTGGAGATACAACT 515  
 673 TCTGCCAAACAAAGCCCTATCCCTATCCACTGGCCCTGGTGTGGAGATACAACT 732

516 GGTTCCTCCGAGTCTGGGATGCTGTGTAAGGCTACTTCCCTGAGTCACTGCTGTG 575  
 733 GGCTCCCTCGGTGACTCTAGGATGCTGTGTAAGGCTATTTCCCTGAGCAGTCACTGTG 792

576 ACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCTCGAGTCT 635  
 793 ACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCTCGAGTCT 852

636 GGACTCTACATATGAGCAGTCTAGTCTGCTCCCTCCAGCAGTGTGCACACCTTCCAGCAGT 695  
 853 GACCTCTACACCTCTCAGCAGTCTAGTCTGCTTAACTCTGAGCAGTGTGCACACCTTCCAGCAGT 912

696 GTCACCTGACGGTGTCTACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 755  
 913 ATCACCCTGCAATGTGGCCCTCCGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 972

756 AGCGGGCCCATTTCAACAATCAACCCCTGTCTCCATGCAAGGAGTGTCAACAAATGCCCA 815  
 973 AGAGGGCC-----ACAATCAAGCCCTGTCTCCATG-----CAAAATGCCCA 1014

816 GCTCCTAACTCGAGGGTGGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 875  
 1015 GCACCTAACCTCTTGGGTGGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1074

876 CTCATGATCTCCCTGACACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 935  
 1075 CTCATGATCTCCCTGACCCCATAGTCAATAGTCAATAGTCAATAGTCAATAGTCAATAGTCAAT 1134

936 CCAGAGCTCCAGATCAGCTGTTTGTGAACAGCTGGAAGTACACACAGCTCAGACACAA 995  
 1135 CCAGATGTTCCAGATCAGCTGTTTGTGAACAGCTGGAAGTACACACAGCTCAGACACAA 1194

996 ACCATAGAGAGGATTACACAGTACTTCCGGGTGGTCAAGCAGCAGCAGCAGCAGCAGCAGCAG 1055  
 1195 ACCATAGAGAGGATTACACAGTACTTCCGGGTGGTCAAGCAGCAGCAGCAGCAGCAGCAGCAG 1254

1056 CAGGACTGGATGAGTGGCAAGAGTTCAAATGCAAGGTCAACACAAAGAGCTCCCAATCA 1115  
 1255 CAGGACTGGATGAGTGGCAAGAGTTCAAATGCAAGGTCAACACAAAGAGCTCCCAAGCG 1314

1116 CCCATCGAGAGACCATCTCAAAATTAAGGGTCAAGGCTAGTCAAGGCTCCCAAGTATACATC 1175  
 1315 CCCATCGAGAGACCATCTCAAAATTAAGGGTCAAGGCTAGTCAAGGCTCCCAAGTATATGTC 1374

1176 TTGCGGCCACAGCAGCAGCTTGTGCAAGAAAGATGTCAAGTCTCACTTGTGCTGCTGCTG 1235  
 1375 TTGCTTCCACCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1434

1236 GGCTTCAACCTTGGAGACATCAGTGTGGAGTGGACCAATGGGCATACAGAGAGAAC 1295  
 1435 GACITTCATGCTGAGACATTTACGTGGAGTGGACCAACAGCGGGAACAGAGCTAAAC 1494

1296 TACAAGGACACGGCACAGTCTCTGAGTCTGAGGTTCTTACTTATATATAGCAAGCTC 1355  
 1495 TACAAGGACACGTAAGTCTCTGAGTCTGAGGTTCTTACTTATATATAGCAAGCTG 1554

1356 ATATGAAACAGCAAGTGGGAGAAACAGATTCTTCTCATGCAAGCTGAGACAGAG 1415  
 1555 AGAGTGGAAAGAGAACTGGGTGGAAAGAAATAGCTACTCTCTGTTCAAGTGGTCCACGAG 1614

1416 GGTCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1471  
 1615 GGTCTGCAATATCAACACAGCTAAGAGCTTCTCCCGGACTCCCGGTAATAGAGC 1670

RESULT 11  
 AAF30341  
 ID AAF30341 standard; cDNA; 6729 BP.  
 XX AAF30341;  
 AC AAF30341;  
 DT 14-MAY-2001 (first entry)  
 XX Bicistronic idiotypic plasmid VR1632.  
 DE Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;  
 KW immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1632;  
 KW antibody; idiotypic; vector; ss.  
 XX Chimeric - Cytomegalovirus.  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Bos taurus.  
 PN WO200109303-A2.  
 XX 08-FEB-2001.  
 PD 31-JUL-2000; 2000WO-US20679.  
 PF 30-JUL-1999; 99US-0146170.  
 PR (VICA-) VICAL INC.  
 XX Hermanson GG;  
 PI WPI; 2001-123319/13.  
 DR Immunogenic compositions comprising Flt-3 ligand encoding  
 PT polynucleotide and one or more antigen, or cytokine encoding  
 PT polynucleotides, useful for suppressing tumour growth and for treating  
 PT autoimmune diseases (e.g. rheumatoid arthritis) -  
 XX Example 2; Page 107-111; 149pp; English.  
 PS The present sequence is that of bicistronic plasmid VR1632, which  
 CC includes the cytomagalovirus immediate-early promoter, enhancer and  
 CC 5' untranslated sequences, driving the expression of mouse  
 CC immunoglobulin kappa light and gamma 1 heavy chain constant  
 CC regions. The transcriptional terminator region includes polyA and  
 CC termination signals from the bovine growth hormone gene.  
 CC Tumour-specific variable regions from a patient can be PCR amplified  
 CC and cloned into this vector to produce the patient's individual  
 CC vaccine construct. The light and heavy chain variable regions from  
 CC the B-cell lymphoma cell line RAMOS were amplified and cloned into  
 CC VR1632 to provide test vaccine construct VR1642 (see AAF30316).  
 CC According to the invention, co-administration of VR1642 with a  
 CC plasmid (see AAF30314) encoding human Fms-like tyrosine kinase  
 CC (Flt-3 ligand) provides a means of treating a patient with B-cell  
 CC lymphoma.  
 XX Sequence 6729 BP; 1727 A; 1744 C; 1629 G; 1629 T; 0 other;  
 SQ Query Match 46.5%; Score 737.8; DB 22; Length 6729;  
 Best Local Similarity 84.3%; Pred. No. 4.7e-171;  
 Matches 861; Conservative 0; Mismatches 142; Indels 18; Gaps 2;

QY 449 CGTCTCCCTCAGCCAAACAAACACCCCATCATCTATCCACTGGCCCTGGTGTGGAGA 508  
 DB 2734 CGTCTCCCTCAGCCAAACAAACAGCGCCCATCGCTATCCACTGGCCCTGGTGTGGAGA 2793

QY 509 TACAAGTGGTCTCCCTCGGTGACTCTGGATGCTGTGCTCAAGGCTACTTCCCTGAGTCACT 568  
 DB 2794 TACAAGTGGTCTCCCTCGGTGACTCTAGGATGCTGTGCTCAAGGCTATTTCCCTGAGCCAGT 2853

QY 569 GACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCTCT 628  
 DB 2854 GACTGTGACTTGGAACTCTGGATCCCTGTCCAGTGTGTGCACACCTTCCAGCTCTCTCT 2913





Db 232 CAACCAUUAUGUUGUGUAGUUAUACACACCUUCCAUCCAGACAGUGUAGAGGGCGCAUUA 291  
QY 292 GCATCAGCAAGGACAAATTCAGAGCCCAACTCTTCTTTAAATGAACAGTCTCGCAGCTA 351  
Db 292 CCAUCCAGAGACAAUGCCAAAGAACACCCUUAUCCUGCAAAUGAGAGUGAGUGUCUG 351  
QY 352 CTGACACAGCAATATATTTACTGTGCGCAAAATAGAGGGGATATTTACTATGATTTCACTT 411  
Db 352 AGGACACGGCCGUAUUAUACUGUGCAAG--CCCCUUAUUAUUGUAGUGGGACU 408  
QY 412 ATGCATGAGTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCTCAGCCCAAAACACAC 471  
Db 409 AUGCAUGGACUACUGGGGUAAGGAACCCAGACACCGUCUCCAGCCAAACAGACAC 468  
QY 472 CCCCATCAGTCTATCCACTGCGCCCTGGGTGTGAGATACAACTGTTCTCCGTGACTC 531  
Db 469 CCCCAUCUGUAUCCAGUGGCCCGUGUAUUGUGCCCAACUAACUCCUAGGUGACCC 528  
QY 532 TGGGATGCTGCTCAAGGGCTACTTCCCTGAGTCAGTGTGACTGTGGAACCTGGAT 591  
Db 529 UGGGAUGCCUGUAAGGCUUUAUCCUGAGCAGUGACAGUGACUUGAACUCUGGAU 588  
QY 592 CCCTGTCCAGCAGTGTGACACACTTCCAGCTTCCTGCTGAGTCTGGACTCTACACTATGA 651  
Db 589 CCUGUCCAGCGUGUGACACACCUUCCAGUGUCCUGCAGUCUACACUCUGA 648  
QY 652 GCAGCTCAGTACTGCTCCCTCCAGCAGCTGGCAAGTCAGACCGTCACTTCGACGCTG 711  
Db 649 GCAGCUGACUGAGUGUCCUCCAGCCUCCGCGCAGCAGCAGCAGCAGCAGCAGCAG 708  
QY 712 CTCACCCAGCAGCAGCAGCAGCTGGTGAACAAAACCTTGAGCCAGCGGGCCCTTTCAA 771  
Db 709 CCCACCCGCGCAGCAGCAGCAGGUGGACAAAGUUGGACAAAGUUGUUGUUGUUGUA 768  
QY 772 CAATCAACCCCTGTCTCTCATGCAAGGAGTGTACAAATGCCAGCTCCTAACCTCGAGG 831  
Db 769 AGCCUUGCAUAG-----UACAGUCCAG 792  
QY 832 GTGACACATCGCTTCTCATCTTCCCTCAATATCAAGGATGTACTATGATCTCCCTGA 891  
Db 793 AAGUAUACUUGUUAUUAUCCUCCCAAGCCAGGAGUGUGUCCACCAUUAUACUCUGA 852  
QY 892 CACCAAGGTCACGT 951  
Db 853 CUCCUAAAGGUCACUGUGUUGUUGUAGACUACAGCAGGAGUAGUCCGAGGUGCUUA 912  
QY 952 GCTGTTTGTGAACACAGCTGGAAGTACACAGCTCAGACACAAACCCATAGAGAGATT 1011  
Db 913 GCUGUUGUUGAUGAUGUGGAGGUGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 972  
QY 1012 ACAACGACTATCTCGGGT 1071  
Db 973 UCAACAGCACUUAUCCGUGCAGUCAGUAGUUAUCCUUAUCCUUAUCCUUAUCCUUA 1032  
QY 1072 GCAAGGATTCATGAGTCAACAAAGACCTCCCATCAACCCATCCATCCATCCATCCAT 1131  
Db 1033 GCAAGGAGUUAUAGUGGAGGUGUACAAAGCAGUUAUCCUCCGCGCAGUUAUCCU 1092  
QY 1132 TCTCAAAATTAAGGCTAGTCAGAGCTCCACAGTATACATCTTCCGCGCCACGAGC 1191  
Db 1093 UCUCCAAAACCAAGGAGCAGACCGAGGUGCAGCAGGUGUACACCAUCCUCCUCCAA 1152  
QY 1192 AGCAGTTGTCCAGGAAGATGTCTAGTCTCACTTCTGCTGTGTGTGTGTGTGTGTGTGT 1251  
Db 1153 AGCAGUCCCAAGGAUUAAGUAGUCUGACUCCUGCAUUAACAGUUAUCCUCCUCCAA 1212  
QY 1252 ACATCAGTGTGGAGTGACCAAGTGGGATACAGAGGAGAGTACAAAGGACACACGAC 1311  
Db 1213 ACAUUAUGUGGAGUGGAGUGGAGUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1272  
QY 1312 CAGTCTCGGAGCTGAGGGTCTTACTTATATATAGAGCTCAATATGAAACAAAGCA 1371  
Db 1273 CCAUUAUGAACAGAAUGGUCUUAUCCUACACAGCAGCAGCAGCAGCAGCAGCAGCAG 1332

QY 1372 AGTGGGAGAAAACAGATCTCTTCTCATGTCAAGCTGAGACACGAGGGTCTGAAAAATTACT 1431  
Db 1333 ACUGGAGGAGCAAAUAUUAUCCUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1392  
QY 1432 ACCTGAAGAAGACCACTCTCCCGGTCTCCGGTAAATGAGCTCAGCACCACCAAGCTCTC 1491  
Db 1393 AUACUGAGAAGAGCCUCCUCCACUCUCCUGUAAAUUAUUAUUAUUAUUAUUAUUAU 1452  
QY 1492 AGTCTCTAAGACACACTGGCACCCTATATCCATGATCTCCCTTGTATATAAATGAATCCAG 1551  
Db 1453 UGGUCCUACAGACUCUGACACUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 1511  
QY 1552 CAAAGCCTGG 1561  
Db 1512 CACUGCCUUG 1521

## RESULT 14

AAN40024

ID AAN40024 standard; DNA; 1528 BP.

XX AC AAN40024;

XX DT 01-DEC-1991 (first entry)

XX DE Combined cDNA inserts of p gamma 298 and p gamma 11 which encode gamma anti-carcinoembryonic antigen chain.

XX KW Immunoglobulin; ds DNA; carcinoembryonic antigen;

XX KW vector p gamma 11; vector p gamma 298.

XX PN EPI25023-A.

XX PD 14-NOV-1984.

XX PF 06-APR-1984; 84EP-0302368.

XX PR 08-APR-1983; 83US-0483457.

XX PA (CITY ) CITY OF HOPE.

XX PA (GETH ) GENENTECH INC.

XX PI Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;

XX DR WPI; 1984-283749/46.

XX PT Immunoglobulin(s) produced by recombinant host cells - useful as antibodies analogous to forms from mammals.

XX PS Disclosure; Fig. 5A-B; 79pp; English.

XX CC The sequence is the combined cDNA inserts of vectors p gamma 298 and p gamma 11. The sequence encodes gamma anti-carcinoembryonic antigen chain. Using the vectors the immunoglobulin is produced readily in pure monoclonal form. Genetic manipulations can be used to produce chimeras of variants drawing their homology from species differing from each other. Protein manipulation is also possible.

XX SQ Sequence 1528 BP; 376 A; 443 C; 370 G; 339 T; 0 other;

## Query Match

Best Local Similarity 44.9%; Score 713.6; DB 5; Length 1528;

Matches 1048; Conservative 0; Mismatches 419; Indels 43; Gaps 4;

QY 55 TCTGCTGGTGACATTTCCCAAGCTGTCTTATCCAGGTGAGCTGAGCAGTCAAGCAGTCAAGCAG 114

Db 52 TTTACCTTGTCCTTGTGTTTAAAGTTTCCAGTGTGAAGTATGCTGGTGGAGTCTGGGG 111

QY 115 CTGCCCTAGTGCAGCCCTCAACAGAGCCTGTCCATCACTGCACAGTCTCTGTTTCTCAT 174

Db 112 GAGTCTTAATGAGGCTGGAGGGTCCCTGGAACCTCTCTGTGCACCTCTGGATTCACTT 171





[illegible]

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Job time : 416.773 secs

Search completed: June 23, 2003, 20:29:03  
Job time : 416.773 secs



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OM nucleic - nucleic search, using sw model

Run On: June 23, 2003, 16:26:36 ; Search time 4270.96 seconds  
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Title: US-09-770-916-1

Perfect score: 1588

Sequence: 1 ccattcttctcatagac.....taaaaaaaaaaaaaaaaaaaaa 1588

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.\*

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3: gb.in.\*

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11: gb.sts.\*

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32: em.htg\_other.\*

33: em.htg\_mus.\*

34: em.htg\_pln.\*

35: em.htg\_rod.\*

36: em.htg\_mam.\*

37: em.htg\_vrt.\*

38: em\_sy.\*

39: em.htgo\_hum.\*

40: em.htgo\_mus.\*

41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1232.2	77.6	1616	10	BC010327	BC010327 Mus muscu
2	1195.8	75.3	1578	10	BC025447	BC025447 Mus muscu
3	1174.2	73.9	1579	10	MMIGE6H	X13188 Mouse mRNA
4	1155.8	72.8	1546	10	MMTMTIIGH	X67210 M.musculus
5	1093.8	68.9	1113	10	MMIGG7	V00799 Mouse mRNA
6	1084	68.3	1389	6	AX466450	AX466450 Sequence
7	1083.4	68.2	1171	10	MUSIGHAK3	L00051 Mus musculu
8	1081.2	68.1	1365	6	AX466448	AX466448 Sequence
9	975	61.4	1653	10	BC018365	BC018365 Mus muscu
10	954.4	60.1	1564	10	BC019489	BC019489 Mus muscu
11	950	59.8	1594	10	BC012207	BC012207 Mus muscu
12	944.4	59.5	1620	10	BC003888	BC003888 Mus muscu
13	940.8	59.2	1570	6	A22261	A22261 M.musculus
14	940.8	59.2	1593	10	BC018535	BC018535 Mus muscu
15	939.2	59.1	1570	6	AR029102	AR029102 Sequence
16	937.6	59.0	1570	6	A77138	A77138 Sequence 6
17	933	58.8	1581	6	A78881	A78881 Sequence 1
18	933	58.8	1581	10	MMIGHQ2AA	X70423 M.musculus
19	932	58.7	1658	10	BC031470	BC031470 Mus muscu
20	925.2	58.3	1584	10	BC003878	BC003878 Mus muscu
21	922.4	58.1	1573	10	BC018280	BC018280 Mus muscu
22	914.6	57.6	1568	6	E33134	E33134 Humanized a
23	889.6	56.0	1410	10	MMU421677	AJ421677 Mus muscu
24	885	55.7	1488	6	AX080953	AX080953 Sequence
25	883.6	55.6	1488	10	D17387	D17387 mRNA for mo
26	821.8	51.8	1095	10	MMIGG6	V00798 Mouse mRNA
27	803.4	50.6	1341	6	I07390	I07390 Sequence 4
28	768.2	48.4	1431	6	AX055011	AX055011 Sequence
29	768.2	48.4	1431	6	AX055012	AX055012 Sequence
30	763.2	48.1	1334	10	RNU39608	U39608 Rattus norv
31	750.2	47.2	1561	10	CMU17166	U17166 Cricetus
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36	731.8	46.1	1523	10	BC008237	BC008237 Mus muscu
37	731.4	46.1	1643	10	BC024405	BC024405 Mus muscu
38	727.6	45.8	1558	10	AF466769	AF466769 Mus muscu
39	720.4	45.4	1572	6	A44967	A44967 Sequence 23
40	720.4	45.4	1572	6	I64458	I64458 Sequence 23
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42	712.8	44.9	1542	10	BC002121	BC002121 Mus muscu
43	705.6	44.4	1505	10	MMACH	X87228 M.musculus
44	703.2	44.3	1517	10	MMU65534	U65534 Mus musculu
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# ALIGNMENTS

RESULT 1	BC010327	BC010327	1616	bp	mRNA	linear	ROD 07-AUG-2002
LOCUS	BC010327	Mus musculus, clone MGC:6533					IMAGE:2651776, mRNA, complete cds.
DEFINITION	BC010327						
ACCESSION	BC010327						
VERSION	BC010327.1	GI:16307556					
KEYWORDS	MGC.						
SOURCE	house mouse.						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
TITLE	1 (bases 1 to 1616)						
JOURNAL	Strausberg, R.						
	Direct Submission						
	Submitted (05-JUL-2001) National Institutes of Health, Mammalian						



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RESULT 2
BC025447
LOCUS      1578 bp      mRNA      linear      ROD 07-AUG-2002
ACCESSION BC025447
VERSION    BC025447.1 GI:19343850
KEYWORDS   MGC.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1578)
Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: qcaps-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 39 Row: P Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
Location/Qualifiers
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/clone="MGC:29400 IMAGE:5068622"
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arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMTV."
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FEATURES
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Best Local Similarity 87.0%; Pred. No. 1.3e-311;
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LOCUS 1113 bp  
DEFINITION  
ACCESSION V00799  
VERSION V00799.1 GI:51837  
KEYWORDS complementary DNA; gamma-immunoglobulin; immunoglobulin.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1113)  
AUTHORS Sikorav,J.L., Auffray,C. and Rougeon,F.  
TITLE Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA  
JOURNAL Nucleic Acids Res. 8 (14), 3143-3155 (1980)  
MEDLINE 81076554  
PUBMED 677755  
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Best Local Similarity 98.9%; Pred. No. 4.7e-284;  
Matches 1101; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
  
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DB 1 GCCAAACAAACACCCCATCAGTCTATCCATCGCCCTGGGTGGAGATACAACATGGT 60  
QY 519 TCCTCGCTGACTCTGGGATGCCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGTGACT 578



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LOCUS	AX466450	Sequence 3 from Patent WO0218443.				
DEFINITION	AX466450					
ACCESSION	AX466450					
VERSION	AX466450.1	GI:218999963				
KEYWORDS		synthetic construct.				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE						
AUTHORS		Esinger,D., Stiles,L., Lamariche,A. and Jelinek,T.				
TITLE		A recombinant monoclonal antibody to phosphotyrosine-containing proteins				
JOURNAL		Patent: WO 0218443-A 3 07-MAR-2002;				
		UPSTATE BIOTECHNOLOGY, INC. (US)				
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## RESULT 7

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ACUS 1171 bp DNA linear ROD 10-MAY-2002
DEFINITION Mus musculus Ig heavy chain variable region gamma-2b C-region gene,
partial cds.
VERSION L00051 J00484 K00698
KEYWORDS L00051.1 GI:194983
SOURCE 3 of 3
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 164 to 1171)
Tucker, P.W., Marcu, K.B., Slightom, J.L. and Blattner, F.R.
Structure of the constant and 3' untranslated regions of the murine
gamma 2b heavy chain messenger RNA
Science 206 (4424), 1299-1303 (1979)
JOURNAL 8081501
MEDLINE 117548
REFERENCE 2 (bases 1 to 163)

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JOURNAL
MEDLINE
PUBMED
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CDS
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QY 553 ACTTCCCTGAGTCACTGCTGACCTTGAACCTTGGATCCCTGTCCAGCAGTGTGCACA 612

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Tucker, P.W., Marcu, K.B., Newell, N., Richards, J., and Blattner, F.R.  
Sequence of the cloned gene for the constant region of murine gamma  
2b immunoglobulin heavy chain  
Science 206 (4424), 1303-1306 (1979)  
8081502  
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3 (bases 1 to 1171)  
Zakut, R., Cohen, J., and Givol, D.  
Cloning and sequence of the cDNA corresponding to the variable  
region of immunoglobulin heavy chain MPC11  
Nucleic Acids Res. 8 (16), 3591-3601 (1980)  
81053741  
6253904  
4 (bases 1 to 1171)  
Zakut, R., Cohen, J.B., and Givol, D.  
Cloning and sequence of the cDNA corresponding to the variable  
region of immunoglobulin heavy chain MPC11  
Nucleic Acids Res. 8, 4839-4839 (1980)  
5 (bases 62 to 466)  
Zakut, R., Cohen, J., and Givol, D.  
Cloning and sequence of the cDNA corresponding to the variable  
region of immunoglobulin heavy chain MPC11  
Nucleic Acids Res. 8 (16), 3591-3601 (1980)  
81053741  
6253904  
The first 53 bp of [2] are a cloning artifact (F.R. Blattner,  
private communication).  
IgG-2b can be either secreted or membrane-bound. The difference  
between the two forms lies in the C-terminal peptides. The secreted  
tail is encoded immediately 3' to the C-gamma-2b-3 domain. The  
membrane-bound tail is encoded about 1.3 kb 3' to the same domain  
and is expressed via alternative mRNA splicing.

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63..>1072
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327 a 343 c 261 g 240 t

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Matches 1099; Conservative
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Db
36 AAGCTCACACATCTCTCTCTTGACGACCAACACACCCCATCAGTCTATCCACTGG 95
QY 493 CCCCTGGGTGGAGATACACTGTTCTCCGTGACTCTGGGATGCCCTGGTCAAGGGCT 552
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VERSION		
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1365 bp DNA linear PAT 16-JUL-2002		

RESULT 8  
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ACCESSION  
VERSION

AX466448	1365 bp	DNA	linear	PAT 16-JUL-2002
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Sequence 1 from Patent WO0218443.

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AX466448.1 GI:21899961

AA400440.1 GI:21899961

[illegible]



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919 GCCCATGTGTCACATGTGTGGTGGTGTGAGCGAGGATGACCCAGAGCTCCAGATCA 978

952 GCTGGTTTGTGAACAAGTGAAGTACACACGCTCAGACACAAACCCATAGAGAGGATT 1011

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ACCESSION	BC019489		
VERSION	BC019489.1	GI:18043008	
KEYWORDS	MGC.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1564)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission		
	Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amge@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.		
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## RESULT 11

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DEFINITION Mus musculus, clone MGC:18977 IMAGE:4007264, mRNA, complete cds.
ACCESSION BC012207
VERSION    BC012207.1 GI:15126551
KEYWORDS   MGC.
SOURCE      house mouse.
ORGANISM   Mus musculus
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            1 (bases 1 to 1594)
            Strausberg, R.
            Direct Submission
            Submitted (06-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

```

Clone distribution: MGC clone distribution information can be found











1256	GGGAAACAGAGCTAAACTACAAGAACTGAAACCACTGCTGGACTCTCTGATGTTCTTAC	1311
1338	TTTCATATATAGCAAGCTCAATATGAAACCAAGCAAGTGGGAGAAACACAGATTCTTCTCA	1397
1316	TTTCATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCC	1375
1398	TGCAACGTGAGACACGAGGGTCTGAAAAATTACTAGCTGAAGAAGACCACTCTCCCGGTCT	1457
1376	TGTTAGTGTGCCAGGGTCTGCAATATCACCACAGCTAAGAGCTTCTCCCGGACT	1435
1458	CCGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCCTAAGAGACACTGGCACCCAT	1517
1436	CCGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCCAAGAGACACCCACACTCAT	1495
1518	ATCCATGATCCCTTGTATATAAATGAAGCATCCAGCAAGAGCTGGTACCATTGTAACAAA	1577
1496	CTCCATGCTTCCCTTGTATATAAATGAAGCAAGCAAGCAAGCTGGGACCACTGTAACAAA	1555
1578	AAAAAAA 1585	
1556	AAAAAAA 1563	
SULT 14		
018535		
CUS		
FINITION		
CBSSON		
RSION		
YWORS		
URCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
REMARK		
MENT		
FEATURES		
source		

Db 738 AGGTGGCAAGAAATTTGAGCCAGAGGCC-----ACAATCAAGCCCTGCTCCAT 791  
Qy 793 GCAAGGAGTGTCAAAATGCCAGCTTAACTCGAGGGTGGACCATCCGCTTCATCT 852  
Db 792 G-----CAATGCCAGCACCTAACCTCTGGTGGACCATCCGCTTCATCT 839  
Qy 853 TCCCTCCAAATATCAAGGATGATCTATGATCTCCCTGACACCCCAAGGTCAAGTGTGG 912  
Db 840 TCCCTCCAAAGATCAAGGATGATCTATGATCTCCCTGAGCCCATGTCATGTCATG 899  
Qy 913 TGGTGGATGTGAGCGAGGATGACCCAGAGTCCAGATCAGCTGGTGTGAAACAGTGG 972  
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Qy 973 AAGTACACAGCTCAGACACAAACCCATAGAGAGGATTAACACAGTACTATCCGGTGG 1032  
Db 960 AAGTACTCACAGCTCAGACACAAACCCATAGAGAGGATTAACACAGTACTATCCGGTGG 1019  
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Qy 1513 CCCATATCCATGATCCTTGTATATAAAGATCCAGCAAGGCTGGTACCATGTAAA 1572  
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Db 1560 AAAAAAAAAAAAAA 1575

RESULT 15  
AR029102  
LOCUS AR029102 1570 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 6 from patent US 5859205.  
ACCESSION AR029102  
VERSION AR029102.1 GI:5941075  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1570)  
AUTHORS Adair, J. Robert., Athwal, D. Singh. and Entage, J. Spencer.  
TITLE Humanised antibodies

JOURNAL Patent: US 5859205-A 6 12-JAN-1999;  
FEATURES Location/Qualifiers  
Source 1. 1570  
BASE COUNT 446 a 443 c 356 g 325 t  
ORIGIN  
Query Match 59.1%; Score 939.2; DB 6; Length 1570;  
Best Local Similarity 77.1%; Pred. No. 2.6e-242;  
Matches 1209; Conservative 0; Mismatches 323; Indels 36; Gaps 4;  
Qy 21 CTCCATCAGAGCATGCTGCTTTGGGGCTGCTTCTGCTGGTGGATATCCCAAGCTGT 80  
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Qy 318 CAACCTCTTTTAAATGAACAGTCTGGAGTCTACTGCACACAGCCATATATTAATCTGTGC 377  
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Qy 798 GAGTGTCAAAATGCCAGCTTAACTTCGAGGGTGGACCATCCGTTCTTATCTTCCCT 857  
Db 784 -----CAATGCCAGACCTTAACTCTTGGTGGACCATCCGTTCTTATCTTCCCT 835  
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1218 CTCACCTGCGCTGCTGGGCTTCAACCCCTGGAGACATCAGTGTGGAGTGGACCGACCAAT 1277  
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1278 GGGCATACAGAGAGAGACTACAGGACACCGCACCAGTCTCGGACCTGACGGTCTTCTTAC 1337  
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1496 CTCATGCTTCCCTTGTATATAAATAAAGCACCAGCAATGGCTGGGACCATGTAAAAAAA 1555  
1578 AAAAAAA 1585  
1556 AAAAAAA 1563

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:53 ; Search time 67.8062 Seconds

(Without alignments)  
1452.530 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLFLCLVTFPSCVLSQ.....RHGLKNYLKKTISRSPGK 478

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	2123	83.2	473	11	Q91205	Q91205 mus musculus
2	2081	81.5	474	11	Q8R3H6	Q8R3H6 mus musculus
3	1721.5	67.5	473	11	Q9D8L4	Q9D8L4 mus musculus
4	1719.5	67.4	473	11	Q99L25	Q99L25 mus musculus
5	1703	66.7	468	11	Q99L31	Q99L31 mus musculus
6	1523.5	59.7	469	11	Q8R3V9	Q8R3V9 mus musculus
7	1471.5	57.7	463	11	Q99L34	Q99L34 mus musculus
8	1456.5	57.1	437	11	Q99L44	Q99L44 mus musculus
9	1409	55.2	471	4	Q8TC77	Q8TC77 homo sapien
10	1362	53.4	473	4	Q8TC63	Q8TC63 homo sapien
11	1049.5	41.1	337	6	Q95M34	Q95M34 equus caball
12	941	36.9	482	11	Q91X92	Q91X92 mus musculus
13	889	34.8	278	11	Q921K1	Q921K1 mus musculus
14	846.5	33.2	597	4	Q9BU10	Q9BU10 homo sapien
15	844	33.1	613	4	Q96EY0	Q96EY0 homo sapien
16	843.5	33.1	597	4	Q9BQ88	Q9BQ88 homo sapien

ALIGNMENTS

RESULT 1

Q91205

ID Q91205 PRELIMINARY; PRT; 473 AA.

AC Q91205

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Hypothetical 51.9 kDa protein.

GN AU044919.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010327; AAH10327.1; -

DR MGD; MGI:2144967; AU044919.

DR InterPro; IPR000345; CytC\_heme\_bind.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig\_3.

DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.

SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 83.2%; Score 2123; DB 11; Length 473;

Best Local Similarity 84.7%; Pred. No. 1.9e-166;

Matches 403; Conservative 25; Mismatches 40; Indels 8; Gaps 3;

QY 4 LGLFCLVTFPSCVLSQVQLKQSGVLPQPSQISITCTVSGFSLTSGVHWVRQSPGK 63

Db 5 LNLVF-LVLILKVGQCEVQLVESGGLVKPGSRKLSCAASGFTFSDYGMHWVRQAPKG 63

QY 64 LEWGLVHSGGDTDYNAFI-SRLSISKDNKSQLFKMNLSRAPDTAIYICARNRGDIY 122

Db 64 LEWVAYINSGGTTIYADTVKGRFTISRDNKNTLFLQMTSLRSEDATMYTCAREL---- 119

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Q96AA6 homo sapien  
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Q8WUK1 homo sapien  
Q96PQ8 homo sapien  
Q96QA6 homo sapien  
Q96KX8 homo sapien  
Q99M22 mus musculus  
Q91Z07 mus musculus  
Q99KA4 mus musculus  
Q96K68 homo sapien  
Q8VEA0 mus musculus  
Q99LA6 mus musculus  
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Q91WR1 mus musculus  
Q91WP5 mus musculus  
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Q8WU38 homo sapien  
Q9NPP6 homo sapien  
Q9DCD9 mus musculus  
Q99NG4 mus musculus  
Q9UP60 homo sapien



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QY 129 MDYWGQCTSVTVSSAKTTPSPVYPLAPCGDGTGSSVTLGCLVKGYFPESVTVTWNSGSL 188
DB 125 FAWGGOTLVTVSRAKTAPSVYPLAPVCGGTGSSVTLGCLVKGYFPPEVTVTWNSGSL 184
QY 189 SSVHFTFPALLOGLYTMSSSVTPSQTWPSQVVAHPASSTVDKKLESPGSTSTI 248
DB 185 SSGVHFTFPALLOGLYTLSSSVTVTSNTPSQITCNVAHPASSTVDKKLEPRVPI-TQ 243
QY 249 NPCPPCKECHKCAPNLEGGPSVFIPPNKIDVLMISLTPKVTCTVVVDSEDDPDVOISW 308
DB 244 NPCPPLKECPPCAAPDLGGPSVFIFPPKIDVLMISLSPMTCTVVVDSEDDPDVQISW 303
QY 309 FVNNVEVHTAQOTTHREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIRTIS 368
DB 304 FVNNVEVHTAQOTTHREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIRTIS 363
QY 369 KIKGLVRAPQVYLLPAPAEOLSRKDVSLTCLVVGNGPDISVEMTSNGHTEENYKDTAPV 428
DB 364 KIRGPRAPQVYLLPAPAEOLSRKDVSLTCLVVGNGPDISVEMTSNGHTEENYKDTAPV 423
QY 429 LPSDGSFYIYSLKLNMTKSKWEKTSFCNVRHGLKNYLLKKTISRSPCK 478
DB 424 LPSDGSFYIYSLKLNMTKSKWEKTSFCNVRHGLKNYLLKKTISRSPCK 473
QY 499L25 PRELIMINARY; PRT; 473 AA.
DB 499L25 PRELIMINARY; PRT; 473 AA.
QY 01-JUN-2001 (TrEMBLrel. 17, Created)
DB 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
QY 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
QY Similar to RIKEN cDNA 1810060009 gene.
DB Similar to RIKEN cDNA 1810060009 gene.
QY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QY NCBI_TaxID=10090;
DB NCBI_TaxID=10090;
QY SEQUENCE FROM N.A.
DB SEQUENCE FROM N.A.
QY Strausberg R.;
DB Strausberg R.;
QY Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC003888; AAH03888.1; -.
QY HSSP; P01842; 7FAB.
DB HSSP; P01842; 7FAB.
QY InterPro; IPR003599; Ig.
DB InterPro; IPR003599; Ig.
QY InterPro; IPR003600; Ig_cl.
DB InterPro; IPR003600; Ig_cl.
QY InterPro; IPR003006; Ig_MHC.
DB InterPro; IPR003006; Ig_MHC.
QY Pfam; PF00047; Ig.
DB Pfam; PF00047; Ig.
QY SMART; SM00409; Ig.
DB SMART; SM00409; Ig.
QY SMART; SM00406; Ig.
DB SMART; SM00406; Ig.
QY SMART; SM00410; IG_Like; 1.
DB SMART; SM00410; IG_Like; 1.
QY PROSITE; PS00290; IG_MHC; UNKNOWN.1.
DB PROSITE; PS00290; IG_MHC; UNKNOWN.1.
QY SEQUENCE 473 AA; 5249 MW; BE9889B7986DA155 CRC64;
DB SEQUENCE 473 AA; 5249 MW; BE9889B7986DA155 CRC64;
Query Match 67.4%; Score 1719.5; DB 11; Length 473;
Best Local Similarity 68.6%; Pred. No. 3.2e-133;
Matches 326; Conservative 58; Mismatches 80; Indels 11; Gaps 6;
QY 6 LFLCLVTFPSCVLSQVQLKQSGPGLVQPSQSLITCTVSGFSLTSYGVHWRQSPQKGL 65
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QY 66 WLGVIW---SGGDTDYNAAFISRLSISKDQSLFVKMNSLRATDTAIYICARNRDIYD 124
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QY 66 WIGYIPRDSQTYKNEKFGKATLTADKSSSAYMQLNSLTSEDSAVCFCSRQ-GSIYYG 124
DB 66 WIGYIPRDSQTYKNEKFGKATLTADKSSSAYMQLNSLTSEDSAVCFCSRQ-GSIYYG 124
QY 125 F-TYAMDYWGQCTSVTVSSAKTTPSPVYPLAPCGDGTGSSVTLGCLVKGYFPESVTVTW 183
DB 125 YGLYFYDYGQCTTVTVSSAKTTPSPVYPLAPCGDGTGSSVTLGCLVKGYFPPEVTVTW 184
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DB 185 NSGSLSSVHTFPALLOGLYTMSSSVTPSQTWPSQVVAHPASSTVDKKLEPSG 244
QY 244 PISTINPCPPCKECHKCAPNLEGGPSVFIFPPNPKIDVLMISLTPKVTCTVVVDSEDDPD 303
DB 245 P-TIKPCPC---KCAPNLLGGPSVFIFPPNPKIDVLMISLTPKVTCTVVVDSEDDPD 298
QY 304 VQISWFWNNVEVHTAQOTTHREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPI 363
DB 299 VQISWFWNNVEVHTAQOTTHREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPI 358
QY 364 ERISKTIGLVRAPQVYLLPAPAEOLSRKDVSLTCLVVGNGPDISVEMTSNGHTEENYK 423
DB 359 ERISKTIGLVRAPQVYLLPAPAEOLSRKDVSLTCLVVGNGPDISVEMTSNGHTEENYK 418
QY 424 DTAPVLDSDGSFYIYSLKLNMTKSKWEKTSFCNVRHGLKNYLLKKTISRSPCK 478
DB 419 NTEPVLSDSGSYFYIYSLKLNMTKSKWEKTSFCNVRHGLKNYLLKKTISRSPCK 473
QY 499L31 PRELIMINARY; PRT; 468 AA.
DB 499L31 PRELIMINARY; PRT; 468 AA.
QY 01-JUN-2001 (TrEMBLrel. 17, Created)
DB 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
QY 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
QY Similar to RIKEN cDNA 1810060009 gene.
DB Similar to RIKEN cDNA 1810060009 gene.
QY Mus musculus (Mouse).
DB Mus musculus (Mouse).
QY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QY NCBI_TaxID=10090;
DB NCBI_TaxID=10090;
QY SEQUENCE FROM N.A.
DB SEQUENCE FROM N.A.
QY Strausberg R.;
DB Strausberg R.;
QY Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC003878; AAH03878.1; -.
QY HSSP; P01842; 7FAB.
DB HSSP; P01842; 7FAB.
QY InterPro; IPR003599; Ig.
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DB InterPro; IPR003006; Ig_MHC.
QY Pfam; PF00047; Ig.
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QY SMART; SM00409; Ig.
DB SMART; SM00409; Ig.
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QY SMART; SM00410; IG_Like; 1.
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QY 6 LFLCLVTFPSCVLSQVQLKQSGPGLVQPSQSLITCTVSGFSLTSYGVHWRQSPQKGL 65
DB 6 VIFFLMAVTVGVNSELVQLQSGAELVRPGASVLSCTASGFIKDSLMHWKQRPQGLE 65
QY 66 WLGVIW---SGGDTDYNAAFISRLSISKDQSLFVKMNSLRATDTAIYICARNRDIY 122
DB 66 WIGYIPRDSQTYKNEKFGKATLTADKSSSAYMQLNSLTSEDSAVCFCSRQ-GSIYYG 120
QY 123 YDTYAMDYWGQCTSVTVSSAKTTPSPVYPLAPCGDGTGSSVTLGCLVKGYFPESVTVT 182
DB 121 YGYGY--DWGQGTITVSSAKTTPSPVYPLAPVCGDGTGSSVTLGCLVKGYFPPEVTVT 178
QY 183 WNSGSLSSVHTFPALLOGLYTMSSSVTPSQTWPSQVVAHPASSTVDKKLEPSG 242
DB 179 WNSGSLSSVHTFPALLOGLYTMSSSVTPSQTWPSQVVAHPASSTVDKKLEPSG 238
QY 243 GPSTINPCPPCKECHKCAPNLEGGPSVFIFPPNPKIDVLMISLTPKVTCTVVVDSEDDPD 302
```





Q9R1A4;  
01-MAY-2000 (TrEMBLrel. 13, Created)  
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
Gammal heavy chain of Mab7 (Fragment).  
IGH-4.  
Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RW "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
antibody (Mab 7, its light and heavy chains) and construction of a  
single chain antibody (scFv).";  
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152372; AAD40243.1; -;  
DR HSSP; P01842; 7FAB.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR003600; Igh-like.  
DR InterPro; IPR003006; Igh-MHC.  
DR InterPro; IPR003596; Igh-V.  
DR Pfam; PF00047; Igh-4.  
DR SMART; SM00406; Igh; 1.  
DR SMART; SM00410; Igh-like; 2.  
DR PROSITE; PS00290; IGH\_MHC; UNKNOWN\_1.  
FT NON\_TER 1  
FT NON\_TER 437  
FT SEQUENCE 437 AA; 48142 MW; 5C3A7BB3E7D697C CRC64;  
Query Match 57.1%; Score 1456.5; DB 11; Length 437;  
Best Local Similarity 61.1%; Pred. No. 1.3e-111;  
Matches 280; Conservative 62; Mismatches 95; Indels 21; Gaps 7;  
QY 21 VOLQSGGLVQPSQSLTCTVSGFSLTSYGVHVRQSPGKLEWLGWVWISGGTDYNA 80  
Db 1 VOLQSGGLVQPSQSLTCTVSGFSLTSYGVHVRQSPGKLEWLGWVWISGGTDYNA 80  
QY 81 AFISRLSISKDNKSQSLFQKFNKSLRATDTAIYCAARNRDIYDYTYAMYWGQTSVTV 140  
Db 61 SVKGFTIYKDKNLSLQMSLSRSEDYAYCA--RGD-----YSA-YWGPGLTVTV 111  
QY 141 SAKTTPSVVPLAPGCGDGTGSSVTLGLVKGYPPESVTVTWNSGSLSSSVHTFPALQ 200  
Db 112 SAKTTPSVVPLAPGSAQAQNSMTVGLCLVKGYPPETVTVTWNSGSLSSSVHTFPALQ 171  
QY 201 SGLYTWSSSVVPSVTPSQTVCVAHPASSTTVDKLEPSGPISTINPCPPCKECHKC 260  
Db 172 SGLYTWSSSVVPSVTPSQTVCVAHPASSTTVDKLEPSGPISTINPCPPCKECHKC 260  
QY 261 PAPNLEGGPSVFIIPPNIKDVLMISLTGKLVVVDSEDDPDVQISWVFNVEHTAQT 320  
Db 223 TVPEVS---SVFIIPKPKDVLITLTTPKVTCCVVVDISKDDPEVQFSWFDVVEHTAQT 279  
QY 321 QTHREDYNSIRVSTLPIQHDWMSGKEFKKVNKDLPSPIERTISKIKGLVRAPOVY 380  
Db 280 QPREQFNSTFSELSPIHQDNLNGEKEKRVNSAFAPIETIKTKGRAPQVY 339  
QY 381 ILPPAEOLSKRDVSLTCLVGFNPGDISVEMTSNGHTEENTKDTAPVLDSDGSFYISK 440  
Db 340 TTPPPKEQMAKDKVSLTCMTIDFPEDITVEQWQNPQAEYKNTQPIMDTDSGYFVSK 399  
QY 441 LNMKTSKWEKTDSPCNVRHGLKNYLLKTIISRPCK 478  
Db 400 LNVOKSNWEAGNTFTCSVHEGLNHHHTKLNLSHPGK 437

RESULT 9

Q8TC77

ID Q8TC77

AC Q8TC77

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 51.8 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RW EMBL; BC024289; AAH24289.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 471 AA; 51791 MW; 3887F4CF588660E CRC64;  
Query Match 55.2%; Score 1409; DB 4; Length 471;  
Best Local Similarity 57.3%; Pred. No. 1.2e-107;  
Matches 275; Conservative 74; Mismatches 115; Indels 16; Gaps 7;  
QY 4 LGLLFC-LVTFPCVLSQVQLQVPSQSLTCTVSGFSLTSYGVHVRQSPGK 62  
Db 3 LGLRWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMNVRQAPGK 62  
QY 63 GLEWLGWVINSGGTDYNAFI-SRLSISDNKSQSLFQKFNKSLRATDTAIYCAARNRDI 121  
Db 63 GLEWVSSMSSSSYIYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDLRL 122  
QY 122 --YDFTYAMYWGQTSVTVSSAKTTPSVVPLAPGCGDGTGSSVTLGLVKGYPPESV 179  
Db 123 TSYWYF----DLWGRGLTVTSASATKGPSPVFPAPSSKTSGGTAALGCLVKDYFPEV 178  
QY 180 TVTWNSGSLSSSVHTFPALQ-SGLYTWSSSVVPSVTPSQTVCVAHPASSTTVDKK 238  
Db 179 TVSWNSGALTSVHTFPALVQLQSSGLISLVSVTVPSSSLGTQYICNVNHPKNTKVDKK 238  
QY 239 LEPSPGISTINPCPPCKECHKC-PAPNLEGGPSVFIIPPNIKDVLMISLTGKLVVVDVS 298  
Db 239 VEPKSCDKT-HTCPP-----CPAPELLGGPSVLEFPKPKDLMISRTPEVTCVVVDVS 291  
QY 299 EDDPDVQISWVFNVEHTAQTQTHREDYNSIRVSTLPIQHDWMSGKEFKCKVNNKD 358  
Db 292 HEDPEVKFKNYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKA 351  
QY 359 LSPPIERTISKIKGLVRAPOVYILPPAEOLSKRDVSLTCLVGFNPGDISVEMTSNGHT 418  
Db 352 LPAPLEKTSKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 411  
QY 419 EENYKDTAPVLDSDGSFYISKVNTKWEKTDSPCNVRHGLKNYLLKTIISRPCK 478  
Db 412 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALNHHYTKQSLSPGK 471  
RESULT 10  
Q8TC63  
ID Q8TC63 PRELIMINARY; PRT; 473 AA.  
AC Q8TC63;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE Hypothetical 52.0 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RW EMBL; BC025985; AAH25985.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;



```
QY 237 KLEPSGPSTIN-PCPP-CKECHKCAPNLEGGSVFIFPPNLIKDVLMISITPKVTCVV 294
DE 11: : 11: : 11: : 11: : 11: : 11: : 11: : 11: : 11: : 11: :
Db 226 ---DSNVQELNVCPCISPTTTPPPSCQ--PSSLQRLPALEDLLGS-DASITCTL 278
QY 295 VDSVDDPDVQLSVFVNNVEVHTAQTQTHREDYNT---IRVSTLPTQHODWMSGKFEK 351
Db 279 NGLRDEGAV-FTW-----EPSTGADAVQKXAVQSCGYSVSSVLPQCAERNWGSASF 332
QY 352 KVNKKDLPSPIERTISKIKGLVRAPOVYIILPPPAEQLSRKD-VSLTCLVGFNPGDISV 410
Db 333 CTVTHPE-SDTLGTIAKVTNTPPQVHLLPSPSEELALNELVSLTCLVRAFNPKEVLV 391
QY 411 EWTNGHTE---ENYKDPAPVL-DG--SYFIYSLNNKTSKWEKTSDFSCNVRHEGLK 464
Db 392 RWL-HGNEELSPESVLPKEPCGEGATYIVTSVLRVSAEINKQGDQYSCWGWHEALP 450
QY 465 NYLKKTTISRSPGK 478
Db 451 MNFTQKTIDRLSGK 464

RESULT 13
QY 921K1 PRELIMINARY; PRT; 278 AA.
Db 921K1
QY 01-DEC-2001 (Tremblrel. 19, Created)
Db 01-DEC-2001 (Tremblrel. 19, Last sequence update)
QY 01-MAR-2002 (Tremblrel. 20, Last annotation update)
Db 01-MAR-2002 (Tremblrel. 20, Last annotation update)
QY Unknown (protein for MGC:18977).
Db Unknown (protein for MGC:18977).
QY Mus musculus (Mouse).
Db Mus musculus (Mouse).
QY Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Db Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QY NCBI_TaxID=10090;
Db NCBI_TaxID=10090;
QY SEQUENCE FROM N.A.
Db SEQUENCE FROM N.A.
QY Strausberg R.;
Db Strausberg R.;
QY Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
Db Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
QY EMBL: BC012207; AAH12207.1; -.
Db EMBL: BC012207; AAH12207.1; -.
QY InterPro: IPR003006; Ig_MHC.
Db InterPro: IPR003006; Ig_MHC.
QY Pfam: PF00047; Ig_2.
Db Pfam: PF00047; Ig_2.
QY SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
Db SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 34.8%; Score 889; DB 11; Length 278;
Best Local Similarity 63.2%; Pred. No. 3.6e-65;
Matches 172; Conservative 37; Mismatches 57; Indels 6; Gaps 4;
QY 6 LLFLVTFPFCVLSQVQLKQSGPGLVQPSQSLTCTVSGFSLTSYGVHVRQSPGKLE 65
Db 6 IILFLVATATGVHSQVQLQPGAEVLKPGASVLSKCRASGYTFTSYWVHWYKRRGGGLE 65
QY 66 WLGI-VSGGDTDYNAAFISRLSISKDNKSKQSLFFKMNLSLRATDTAIYCARNGDIYD 124
Db 66 WIGNINPNSGNTWNEKFKKATLAVDKSSSTVIMQLSSLTSEDSAVYYCTRGYG---YD 122
QY 125 FTYAMDVGOGTSTVTVSSAKTTPPSVPLAPGCGDTTGSSVTGLCLVKGYFPEPVITWN 184
Db 123 DVY-FDWGAGTGVTVSSAKTTPPSVPLAPGCGDTTGSSVTGLCLVKGYFPEPVITWN 181
QY 185 SGLSSVHTFPALLOSLGYLTMSSSVTPSPQVTCVAHPASSTTVDRKLEPSGP 244
Db 182 SGLSSGVHTFPALLOSLGYLTMSSSVTPSPQVTCVAHPASSTTVDRKLEPSGP 241
QY 245 ISTINPCPKCKECHKCAPNLEGGSPVIFPP 276
Db 242 I-TQNPCLPKCKECHKCAPNLEGGSPVIFPP 272

RESULT 14
QY 9BUI0 PRELIMINARY; PRT; 597 AA.
Db 9BUI0
QY 01-JUN-2001 (Tremblrel. 17, Created)
Db 01-JUN-2001 (Tremblrel. 17, Created)
```

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DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 65.3 kDa protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002963; AAH02963.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_5.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IGC1; 4.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG-like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 33.2%; Score 846.5; DB 4; Length 597;
Best Local Similarity 34.6%; Pred. No. 3.5e-61;
Matches 203; Conservative 88; Mismatches 180; Indels 115; Gaps 19;
QY 1 MAVLGLEFCLVTFPFCVLSQVQLKQSGPGLVQPSQSLTCTVSGFSLTSYGVHVRQSP 60
Db 1 MKHLWFELLVAAPRWLSQVQLQWAGLLKPKSETLSLTGCVYGGSGYVWSWIRQPP 60
QY 61 KGLEWLGVWGGDTDYNAAFISRLSISKDNKSKQSLFFKMNLSLRATDTAIYCAR--NR 118
Db 61 KGLEWIGEINHSGSTNYNPSLKSRTISVDTSKQLSKLSSVNAADTAVYICARVTR 120
QY 119 GDYYDYFTYANDYWGQTSVTVSSAKTTPPSVYPLAPGCGDTTG--SSVTGLCLVKGYFP 176
Db 121 ASPGTDGRYGMVVGQGTVTVSSGASAPTLFPLV-SCENSPSDTSSVAVGCLAQDFLP 179
QY 177 ESVTVTW--NSGSLSSSVHTFPALLOSLGYLTMSSSVTPSPQVTCVAHP-- 229
Db 180 DSITFSWKYKNNDSISSTRGFPVLRGKYAATSQVLLPSKDVMOGTDEHVYVCKVQHPNG 239
QY 230 ----- 229
Db 240 NKEKNVPLVIAELPPKVSVPVPRDGFPGNPKSLICQATGFSPTQVSWLREGKQV 299
QY 230 ASSTTVDK---KLEPSGPIS-----TINPCP-----PCKECHK-----CP 261
Db 300 GSGVTTDQVQAEAKESGFTYKVTSLTIKESDWLSQSMFTCRVDHRLGLTQQNASSMC- 358
QY 262 APNLEGGSPVIFPPNLIKDVLMISITPKVTCVVDVSEDDPDVOISWPNV--VEVHTA 318
Db 359 VPQDQTAIRFAIPPSFASIFLTKST-KLTLVTLDTLYD-SVTISWTRQNGEAVKHTN 416
QY 319 QTOFHREDYNTIRVSTLPTQHODWMSGKFEKCKVNNKDLPSPIERTISKIKGL-VRAP 377
Db 417 ISESH-----NATFSVAGEASICEDDDWNSGERFTCTVTHTDLPSPKQTSRPGVALRP 473
QY 378 QVYILPPPAEOLS-RKDVSLTCLVGFNPGDISVEWTSNGH--TEENAKDTPAVLD--SD 432
Db 474 DVYLLPPAREQLNRESATITCLVTGFSPADVFQWMQRGQPLSPKQTSRPGVALRP 473
QY 433 GSYFIYSLNNKTSKWEKTSDFSCNVRHEGLKKNYLLKKTISRSPGK 478
Db 534 GRVFAHSILVSEEWNTGYTCVVAHEALPNRVTERTVKDKSTGK 579
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```
SULT 15
6EYO Q96EYO PRELIMINARY: PRT: 613 AA.
Q96EYO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:20337).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=B-CELL;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC011857; AAH11857.1; -
InterPro; IPR003598; IG_C2.
InterPro; IPR003006; IG_MHC.
Pfam; PF00047; Ig_5.
SMART; SM00408; IGC2; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Immunoglobulin domain.
SEQUENCE 613 AA: 67273 MW; 31214203FB8421E7 CRC64;

Query Match 33.1%; Score 844; DB 4; Length 613;
Best Local Similarity 34.4%; Pred. No. 5.8e-61;
Matches 200; Conservative 93; Mismatches 171; Indels 118; Gaps 19;

1 NAVLGLLFCLVTFPCVLSQVOLKSGPGLVQPSQSLTCTVSGFSLTSYGVHVRQSP 60
  |||||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1 MKHLWFFLLVAAPRWLSQVOLQESGPLVKPSETLSLTCTVSGGSISSYVWSWIRQPA 60
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61 GKLEWLVGIVSGGTDYNAFISLSISKONSKSOLFCKMNSLRATDTAIYYCARNRGD 120
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61 GKLEWIGRIYTSSTNTNPSLKSRTVSDTSKNQFSLKSSVTAADTAIVYCASQWPE 120
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
121 IYDFTYAMDYWGQGTSTVTSAKTTPPSVPLAP---CGDITGSSVTLGCLVRGYFPE 177
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
121 LP---TVGLFWGQGLTLTVSSGSASAPTLPLVSCENSPSDT--SSVAVGCLAQDFLPD 175
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
178 SVTVTW---NSGSLSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQT---VTCVAHP--- 229
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
176 SITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVLLPSKDVMOGTDHVVCKVQHPNGN 235
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
230 -----A 230

236 KEKNVLPVIAELPPKVSFVPPRDGFFGNPRKSKLICQATGFSRQIQVSWLREGKQVG 295
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
231 SSTTVDK---KLEPSGPIS-----TINPCP-----PCKECKH-----CPA 262
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
296 SGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMETCRVDHRLGLTFQONASSMC-V 354
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
263 PNLGGPSVFIPFPKIDVLMISLPKVCVVVDSEDDPDVQISVFNVN---VEVHTAQ 319
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
355 PQDDTAIRVAIRPFPFASIFLKST-KLTCLTDLTYD-SVTISWTRONGEAVKTHNI 412
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
320 TQTHREDYNSTIRVSTLPIQHDNMSGKEFKCKVNKNKDLPSPIERTISKIKGL-VRAPO 378
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
413 SESHP---NATFSAVEASICEDDNNNGSERFTCTVTHDLPSPKLTISRPKGVALLHRPD 469
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
379 VYILPPPAQOLS-RKDVSLTCLVWGNPGDISVEWTSNGH--TEENYKDTAPVLD--SDG 433
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
470 VYLLPPAREQLNRESATITCLVTGFSPADVFQWMQRGQPLSPKPKYVTSAPMPEQAPG 529
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
434 SYFIYSKLNKTSKWEKTSFSCNVREHGLKNYLLKTKTISR 475
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
530 RYFAHSILTVEEENWTGETYTCWAHEALPNRVTERTVDKS 571
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:52 ; Search time 19.4691 Seconds  
(without alignments)  
1018.315 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 252

Sequence: 1 MAVGLLFLVFPSCVLSQ.....RHEGLKNTYKKTISRSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	70.6	336	1	GCB_MOUSE
2	1797	70.4	405	1	GCB_MOUSE
3	1419	55.6	330	1	GCAA_MOUSE
4	1414	55.4	399	1	GCAH_MOUSE
5	1385.5	54.3	335	1	GCAH_MOUSE
6	1326.5	52.0	333	1	GCB_MOUSE
7	1202.5	47.1	329	1	GCB_MOUSE
8	1170	45.8	329	1	GCB_MOUSE
9	1159	45.4	398	1	GCB_MOUSE
10	1150	45.1	324	1	GCB_MOUSE
11	1145	44.9	393	1	GCB_MOUSE
12	1112	43.6	326	1	GCB_MOUSE
13	1100	43.1	322	1	GCA_MOUSE
14	1087	42.6	330	1	GCB_MOUSE
15	1080.5	42.3	323	1	GCB_MOUSE
16	1080.5	42.3	329	1	GCB_MOUSE
17	1059	41.5	326	1	GCB_MOUSE
18	1054.5	41.3	327	1	GCB_MOUSE
19	777.5	30.5	290	1	GCB_MOUSE
20	584	22.9	116	1	HV45_MOUSE
21	556	21.8	144	1	HV43_MOUSE
22	502	19.7	115	1	HV44_MOUSE
23	478	18.7	454	1	MUC_MOUSE
24	477.5	18.7	429	1	EPC_MOUSE
25	474	18.6	421	1	EPC_MOUSE
26	473	18.5	428	1	EPC_MOUSE
27	442.5	17.3	438	1	HVC2_MOUSE
28	437.5	17.1	370	1	HVC1_MOUSE
29	435.5	17.1	438	1	HVC3_MOUSE
30	432.5	16.9	458	1	MUC_MOUSE
31	429	16.8	391	1	MUC_MOUSE
32	426.5	16.7	393	1	MUC_MOUSE
33	425.5	16.7	461	1	HVC4_MOUSE

34	422.5	16.6	479	1	MUC_MOUSE
35	420	16.5	450	1	MUC_MOUSE
36	417	16.3	457	1	MUC_MOUSE
37	402.5	15.8	353	1	ALC1_MOUSE
38	397	15.6	135	1	HV02_MOUSE
39	387	15.2	340	1	ALC2_MOUSE
40	383.5	15.0	137	1	HV46_MOUSE
41	383.5	15.0	353	1	ALC1_MOUSE
42	380	14.9	344	1	ALC_MOUSE
43	372.5	14.6	454	1	MUC_MOUSE
44	372.5	14.6	455	1	MUC_MOUSE
45	362.5	14.2	476	1	MUC_MOUSE

## ALIGNMENTS

RESULT 1					
GCB_MOUSE					
ID	GCB_MOUSE	STANDARD;	PRT;	336 AA.	
AC	P01866;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ig gamma-2B chain C region.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A. (A ALLELE).				
RX	MEDLINE=80120716; PubMed=6766534;				
RA	Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;				
RT	"Complete nucleotide sequence of immunoglobulin gamma2b chain gene				
RT	cloned from newborn mouse DNA.";				
RL	Nature 283:786-789(1980).				
RN	[2]				
RP	SEQUENCE FROM N.A. (MPC 11).				
RX	MEDLINE=80081501; PubMed=117548;				
RA	Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;				
RT	"Structure of the constant and 3' untranslated regions of the murine				
RT	gamma 2b heavy chain messenger RNA.";				
RL	Science 206:1299-1303(1979).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=80081502; PubMed=117549;				
RA	Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;				
RT	"Sequence of the cloned gene for the constant region of murine gamma				
RT	2b immunoglobulin heavy chain.";				
RL	Science 206:1303-1306(1979).				
RN	[4]				
RP	SEQUENCE FROM N.A. (B ALLELE).				
RX	MEDLINE=82173203; PubMed=6803173;				
RA	Ollio R., Rougeon F.;				
RT	"Mouse immunoglobulin allotypes: post-duplication divergence of gamma				
RT	2a and gamma 2b chain genes.";				
RL	Nature 296:761-763(1982).				
RN	[5]				
RP	CARBOHYDRATE-LINKAGE SITE THR-105.				
RX	MEDLINE=94216359; PubMed=7512967;				
RA	Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,				
RA	Irimura T., Takahashi N., Kato K., Arata Y.;				
RT	"O-glycosylation in hinge region of mouse immunoglobulin G2b.";				
RL	J. Biol. Chem. 269:12345-12350(1994).				
CC	MODIFIED WITH 2 SIALIC ACID RESIDUES.				
CC	!- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS				
CC	MODIFIED WITH 2 SIALIC ACID RESIDUES.				
CC	!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA				
CC	CHAINS.				
CC	!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.				
DR	PIR: A02157; G2MS11.				
DR	HSSP: P01842; 7FAB.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003597; Ig-cl.				

P04221	Oryctolagus
P01874	canis famil
P20768	suncus muri
P20758	gorilla gor
P20957	xenopus lae
P01877	homo sapien
P01822	mus musculu
P01876	homo sapien
P01878	mus musculu
P06337	mesocricetu
P01872	mus musculu
P01873	mus musculu

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InterPro: IPR003600; Ig_Like.
Pfam: PF00047; Ig_3.
SMART: SM00410; Ig_Like; 1.
SMART: SM00407; IgC1; 2.
PROSITE: PS00290; Ig_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
NON_TER 1
DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 150 210
DISULFID 256 314
CARBOHYD 105 105 O-LINKED (GALNAc...).
MOD_RES 336 336 REMOVED POST-TRANSLATIONALLY (PROBABLE).
VARIANT 163 163 Q -> R (IN B ALLELE).
VARIANT 194 194 T -> A (IN B ALLELE).
VARIANT 300 300 N -> D (IN B ALLELE).
VARIANT 301 301 M -> I (IN B ALLELE).
VARIANT 25 25 L -> S (IN REF. 2 AND 3).
CONFLICT 36 36 S -> P (IN REF. 2 AND 3).
CONFLICT 239 239 I -> T (IN REF. 2 AND 3).
SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;

Query Match 70.6%; Score 1802; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.2e-120; Indels 0; Gaps 0;
Matches 336; Conservative 0; Mismatches 0;

143 AKTTPSVYPLAPGCGDTTGSSTVTLGCLVKGFFPESVTVTWNSGSLSSSVHFFPALQSG 202
|||||
1 AKTTPSVYPLAPGCGDTTGSSTVTLGCLVKGFFPESVTVTWNSGSLSSSVHFFPALQSG 60

203 LYTMSSSVTPSPSTWPSQVTCTCSVAHPASSTVTDKLEPSGPISTINPCPCKECHKCPA 262
|||||
61 LYTMSSSVTPSPSTWPSQVTCTCSVAHPASSTVTDKLEPSGPISTINPCPCKECHKCPA 120

263 PNLEGGPSVFIIPPNIKDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 322
|||||
121 PNLEGGPSVFIIPPNIKDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 180

323 HREDNSTIRVYSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 382
|||||
181 HREDNSTIRVYSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 240

383 PPPAQQLSRKDVSLTCLVVGFPNGDISVWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
|||||
241 PPPAQQLSRKDVSLTCLVVGFPNGDISVWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300

443 MKTSKWKETDSCNVRHGLKNYLLKTIISRPCK 478
|||||
301 MKTSKWKETDSCNVRHGLKNYLLKTIISRPCK 336

RESULT 2
GBM_MOUSE STANDARD; PRT; 405 AA.
P01867:
21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE OF 335-405 FROM N.A.
MEDLINE=8222190; PubMed=6283537;
Yamawaki-kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
```

```
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
[2]
SEQUENCE OF 335-378 FROM N.A.
MEDLINE=82115295; PubMed=6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
Cell 26:19-27(1981).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
-!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
CHAINS.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
-!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
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or send an email to license@isb-sib.ch).
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EMBL: J00462; AAB59659.1; ALT_INIT.
PIR: C02154; G2MSBM.
HSSP: P01842; 7FAB.
MGD: MGI:96445; Ig-h-3.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig-CL.
InterPro: IPR003600; Ig_Like.
Pfam: PF00047; Ig_3.
SMART: SM00410; Ig_Like; 1.
SMART: SM00407; IgC1; 2.
PROSITE: PS00290; Ig_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
Alternative splicing.
NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 15 15 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 150 210
DISULFID 256 314
TRANSMEM 352 369 POTENTIAL.
DOMAIN 370 405 CYTOPLASMIC (POTENTIAL).
SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;

Query Match 70.4%; Score 1797; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.6e-120; Indels 0; Gaps 0;
Matches 335; Conservative 0; Mismatches 0;

QY 143 AKTTPSVYPLAPGCGDTTGSSTVTLGCLVKGFFPESVTVTWNSGSLSSSVHFFPALQSG 202
|||||
Db 1 AKTTPSVYPLAPGCGDTTGSSTVTLGCLVKGFFPESVTVTWNSGSLSSSVHFFPALQSG 60
|||||
QY 203 LYTMSSSVTPSPSTWPSQVTCTCSVAHPASSTVTDKLEPSGPISTINPCPCKECHKCPA 262
|||||
Db 61 LYTMSSSVTPSPSTWPSQVTCTCSVAHPASSTVTDKLEPSGPISTINPCPCKECHKCPA 120
|||||
QY 263 PNLEGGPSVFIIPPNIKDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 322
|||||
Db 121 PNLEGGPSVFIIPPNIKDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 180
|||||
QY 323 HREDNSTIRVYSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 382
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Db 181 HREDYNSTIRVVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240

QY 383 PPABQLSRKDVSLCLVGVGNPDISVWTSNGHTEENYKDTAPVLDSDGSGYFIYSKLN 442

Db 241 PPABQLSRKDVSLCLVGVGNPDISVWTSNGHTEENYKDTAPVLDSDGSGYFIYSKLN 300

QY 443 MKTSKWKTDSCNVRHEGLKNYLYKKTISRSPG 477

Db 301 MKTSKWKTDSCNVRHEGLKNYLYKKTISRSPG 335

RESULT 3

SCAA\_MOUSE

ID GCAM\_MOUSE STANDARD; PRT; 330 AA.

AC P01863;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 19, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Ig gamma-2A chain C region, A allele.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI\_TaxID=10090;

[1]

SEQUENCE FROM N.A.

MEDLINE=81076554; PubMed=6777755;

Sikora J.-L., Auffray C., Rougeon F.;

"Structure of the constant and 3' untranslated regions of the murine

Balb/c gamma 2a heavy chain messenger RNA.";

Nucleic Acids Res. 8:3143-3155(1980).

[2]

SEQUENCE FROM N.A.

MEDLINE=81198976; PubMed=6262729;

Yamawaki-Kataoka Y., Miyata T., Honjo T.;

"The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene

and evolution of heavy chain genes: further evidence for intervening

sequence-mediated domain transfer.";

Nucleic Acids Res. 9:1365-1381(1981).

[3]

SEQUENCE FROM N.A.

MEDLINE=81223894; PubMed=6787604;

Ollio R., Auffray C., Morchamps C., Rougeon F.;

"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes

suggests that exons can be exchanged between genes in a multigenic

family.";

Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).

[4]

MYELOMA PROTEIN MOPC 173.

MEDLINE=74175517; PubMed=4831970;

Bourgeois A., Fougereau M., Rocca-Serra J.;

"Determination of the primary structure of a mouse IgG2a

immunoglobulin: amino-acid sequence of the Fc fragment. Implications

for the evolution of immunoglobulin structure and function.";

Eur. J. Biochem. 43:423-435(1974).

[5]

DISULFIDE BONDS.

MEDLINE=73056887; PubMed=4565406;

de Preval C., Fougereau M.;

"Determination of the primary structure of a mouse gamma G2a

immunoglobulin. Identification of the disulfide bridges.";

Eur. J. Biochem. 30:452-462(1972).

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entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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EMBL; V00798; CAA24178.1; -

PIR; A02152; G2MSA.

HSP; P01842; 7FAB.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003597; Ig\_cl.

DR InterPro: IPR003600; Ig\_like.

DR Pfam: PF00047; ig; 2.

DR SMART: SM00410; Ig\_like; 1.

DR SMART: SM00407; Igcl; 2.

DR PROSITE: PS00290; IG\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON\_TER 1 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.

SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 55.6%; Score 1419; DB 1; Length 330;

Best Local Similarity 78.6%; Pred. No. 1.6e-93;

Matches 264; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 143 AKTTPSVVYPLAPGCGDTTSSVTGLCLVKGYPESVTVTNWSSGSLSSSVHTFPALQSG 202

Db 1 AKTTPSVVYPLAPGCGDTTSSVTGLCLVKGYPESVTVTNWSSGSLSSSVHTFPALQSG 60

QY 203 LYTMSSSVTPSSTWPSQVTCVAHPASSTVVDKLEPSGPISTINPCPPCKECHKCPA 262

Db 61 LYTLSSSVTVSTWPSQVTCVAHPASSTVVDKLEPSGPISTINPCPPCKECHKCPA 114

QY 263 PNLEGGPSVFIFPPNKKDVLMLSLTPKVTGVVVDVSEDDPDVQISWVFNVEVHTAQTOT 322

Db 115 PNLLGGPSVFIFPPNKKDVLMLSLTPKVTGVVVDVSEDDPDVQISWVFNVEVHTAQTOT 174

QY 323 HREDYNSTIRVVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382

Db 175 HREDYNSTIRVVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 234

QY 383 PPABQLSRKDVSLCLVGVGNPDISVWTSNGHTEENYKDTAPVLDSDGSGYFIYSKLN 442

Db 235 PPPEEMTKQVTLTCMVTFDFMPEDIIYVWNTNGKTELKNTPEVLDSDGSGYFIYSKLR 294

QY 443 MKTSKWKTDSCNVRHEGLKNYLYKKTISRSPG 478

Db 295 VEKKWVVERNSYSCSVVHGLEHNNHTKTSFSTPGK 330

RESULT 4

GCAM\_MOUSE

ID GCAM\_MOUSE STANDARD; PRT; 399 AA.

AC P01865;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-2A chain C region, membrane-bound form.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI\_TaxID=10090;

[1]

SEQUENCE FROM N.A.

MEDLINE=8222190; PubMed=6283537;

Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

"Nucleotide sequences of gene segments encoding membrane domains of

immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA

GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-

BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED

IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND

SEGMENT OF MU CHAINS.

!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.

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EMBL; J00471; AAB59661.1; ALT\_INIT.

PIR; A02154; G2MSAB.

HSSP; P01842; 7FAB.

MGI; 96443; Igh-1.

InterPro; IPR003006; Ig\_MHC.

InterPro; IPR003597; Ig\_C1.

InterPro; IPR003600; Ig\_Like.

Pfam; PF00047; Ig\_2.

SMART; SM00410; Ig\_Like; 1.

SMART; SM00410; Ig\_C1; 2.

PROSITE; PS00290; Ig\_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.

NON\_TER 1

DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 144 204

DISULFID 250 308

DISULFID 346 363

DOMAIN 364 399

CARBOHYD 180 180

SEQUENCE 399 AA; 44020 MW; 4C38138BFAEDJFF0 CRC64;

Query Match 55.4%; Score 1414; DB 1; Length 399;

Best Local Similarity 78.5%; Pred. No. 4.7e-93;

Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

143 AKTTPSVVPLAPCGDITGSSVTLGCLVKGYPESVTVTNWSSGSLSSVHFPALQSG 202

1 AKTAPSVVPLAPVCGDITGSSVTLGCLVKGYPPEVPTLTWNSGSLSSVHFPALQSD 60

203 LYTMSVVTPSPSTWPSQVTCVAHPASSTVVDKLEPGSPITINPCPKCKECHKCPA 262

61 LYTSSVVTPSTWPSQVTCVAHPASSTVVDKLEPGSPITINPCPKCKECHKCPA 114

263 PNLEGGPSVFIFPPNPKIDVLMISLTPKVCVVDVSEDDPDVQISWFNVEVHTAQOT 322

115 PNLEGGPSVFIFPPNPKIDVLMISLTPKVCVVDVSEDDPDVQISWFNVEVHTAQOT 174

323 HREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382

175 HREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 234

383 PPPAEQLSRKDVSLTCLVGFNPGDISVETNSGHTTEENYKDTAPVLDSGVSFYISKLN 442

235 PPPAEEMTKKQVLTCTCMVDFMPEDIVYENNGKTELTAKNTEPVLDSGVSFYISKLR 294

443 MKTSKWEKTDSPSCNVRHGLKNYLLKTKTSRSPG 477

295 VEKKNNVERNYSVCSVVHGLHNHHTTKTSRTPG 329

RESULT 5

CAB\_MOUSE

D CCAB\_MOUSE

C P01864;

T 21-JUL-1986 (Rel. 01, Created)

T 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-2A chain C region, B allele.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=82037861; PubMed=6170065;  
RA SCHREIER P.H., BOTHWELL A.L.M., MUELLER-HILL B., BALTIMORE D.;  
RT "Multiple differences between the nucleic acid sequences of the  
IGG2A and IGG2B alleles of the mouse."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=82037777; PubMed=6794027;  
RA DOGININ M.J., LAUWERYS M., STROBERG A.D.;  
RT "Multiple amino acid substitutions between murine gamma 2a heavy  
chain Fc regions of Igla and Iglb allotypic forms."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).  
CC !- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,  
FROM BALB/C MICE, AT 15% OF THE POSITIONS.  
CC  
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CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -  
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS  
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY  
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL  
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CC OR SEND AN EMAIL TO [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; J00479; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A02153; G2MSAB.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00410; Ig\_Like; 1.  
DR SMART; SM00410; Ig\_C1; 2.  
DR PROSITE; PS00290; Ig\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region.  
KW NON\_TER 1  
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;  
SQ  
Query Match 54.3%; Score 1385.5; DB 1; Length 335;  
Best Local Similarity 77.1%; Pred. No. 3.9e-91;  
Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;  
QY 143 AKTTPSVVPLAPCGDITGSSVTLGCLVKGYPESVTVTNWSSGSLSSVHFPALQSG 202  
DB 1 AKTAPSVVPLAPVCGDITGSSVTLGCLVKGYPPEVPTLTWNSGSLSSVHFPALQSG 60  
QY 203 LYTMSVVTPSPSTWPSQVTCVAHPASSTVVDKLEPGSPITINPCPKCKECHKCPA 262  
DB 61 LYTSSVVTPSTWPSQVTCVAHPASSTVVDKLEPGSPITINPCPKCKECHKCPA 119  
QY 263 PNLEGGPSVFIFPPNPKIDVLMISLTPKVCVVDVSEDDPDVQISWFNVEVHTAQOT 322  
DB 120 PDLGGPSVFIFPPNPKIDVLMISLTPKVCVVDVSEDDPDVQISWFNVEVHTAQOT 179  
QY 323 HREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382  
DB 180 HREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 239  
QY 383 PPPAEQLSRKDVSLTCLVGFNPGDISVETNSGHTTEENYKDTAPVLDSGVSFYISKLN 442  
DB 240 PPPAEEMTKKQVLTCTCMVDFMPEDIVYENNGKTELTAKNTEPVLDSGVSFYISKLR 299  
QY 443 MKTSKWEKTDSPSCNVRHGLKNYLLKTKTSRSPG 478  
DB 300 VQKSTWERSLGFACSVVHGLHNHHTTKTSRSLGK 335



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AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RL region cDNA: extensive homology to mouse gamma 3.1";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
DR EMBL; X07189; CA30169.1; -
DR PIR; S00847; S00847.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match
Best Local Similarity 47.1%; Score 1202.5; DB 1; Length 329;
Matches 229; Conservativity 35; Mismatches 65; Indels 7; Gaps 4;

QY 143 AKTTPSVYPLAPGCGDITGSSVTLGCLVKGYFPEPVTVWNSGSLSSVHTFPAALQSG 202
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ARTTAPSVYPLVPGCGSGTSGSLVTLGCLVKGYFPEPVTVWNSGSLSSVHTFPAALQSG 60

QY 203 LYTWSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSGPISTINPCPCKECHKCPA 262
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 LYTLSSSVTVPSSTWSSQTVTCVAHPASSTVDKLEPSGPISTINPCPCKECHKCPA 114

QY 263 PNLEGGPSVFIIPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWFVNNVEVHTAQOT 322
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115 DNL-GRPSVFIIPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWFVNNVEVHTAQOT 173

QY 323 HREDYNSTIRVVSTLPTQHDWMSGKFEKCKVNNKDLPSPIERTISKTLGLVRAPOVYL 382
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
174 HEEQLNGTFRVSVTLHQLQHDWMSGKFEKCKVNNKDLPSPIERTISKTLGLVRAPOVYL 233

QY 383 PPPAEQLSRKDVSLTCLVGFNPGDISVETNSGHTENYKDTAPVLDSGSGFYISKLN 442
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
234 PPPAEQSKNKVSLTCLVGFNPGDISVETNSGHTENYKDTAPVLDSGSGFYISKLN 293
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```
RESULT 6
CCB_RAT STANDARD; PRT; 333 AA.
ID ID CCB_RAT
P20761; AC
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
RL PIR; PS0018; PS0018.
RL HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match
Best Local Similarity 52.0%; Score 1326.5; DB 1; Length 333;
Matches 248; Conservativity 34; Mismatches 50; Indels 5; Gaps 3;

QY 143 AKTTPSVYPLAPGCGDITGSSVTLGCLVKGYFPEPVTVWNSGSLSSVHTFPAALQSG 202
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 AQTTPSVYPLAPGCGDITGSSVTLGCLVKGYFPEPVTVWNSGSLSSVHTFPAALQSG 60

QY 203 LYTWSSSVTVPSSTWPSQTVTCVAHPASSTVDKLE-PSGPISTINPCPCKECHKCP 261
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 LYTLSSSVTVPSSTWSSQTVTCVAHPASSTVDKLEPSGPISTINPCPCKECHKCP 116

QY 262 APNLEGGPSVFIIPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWFVNNVEVHTAQOT 321
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 VPELGGPSVFIIPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWFVNNVEVHTAQOT 176

QY 322 THREDYNSTIRVVSTLPTQHDWMSGKFEKCKVNNKDLPSPIERTISKTLGLVRAPOVYL 381
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
177 PREEQYNSTRVSVTLPTQHDWMSGKFEKCKVNNKDLPSPIERTISKTLGLVRAPOVYL 236

QY 382 LPPAEQLSRKDVSLTCLVGFNPGDISVETNSGHTENYKDTAPVLDSGSGFYISKLN 441
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
237 MGPPTEQLTQTSVTLTCLVGFNPGDISVETNSGHTENYKDTAPVLDSGSGFYISKLN 296

QY 442 NMKTSKWEKTDSCNVRHGLKNLYLKKLTISRSPGK 478
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 NVESRSDSRAPFCVSVVHGLHNNHHEKSTSRPPGK 333

STANDARD; PRT; 329 AA.
ID ID CCB_RAT
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```

RESULT 11
:IML_MOUSE
: ) GCIM_MOUSE STANDARD; PRT; 393 AA.
: ) P01869;
: 21-JUL-1986 (Rel. 01, Created)
: 01-AUG-1991 (Rel. 19, Last sequence update)
: 30-MAY-2000 (Rel. 39, Last annotation update)
: Ig gamma-1 chain C region, membrane-bound form.
: Mus musculus (Mouse).
: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
: NCBI_TaxID=10090;
: [1]
: SEQUENCE FROM N.A.
: MEDLINE=80045036; PubMed=115593;
: Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
: Takahashi N., Mano Y.;
: "Cloning and complete nucleotide sequence of mouse immunoglobulin
: gamma 1 chain gene.";
: Cell 18:559-568(1979).
: [2]
: SEQUENCE OF 323-393 FROM N.A.
: MEDLINE=82197626; PubMed=6804950;
: Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
: "mRNA for surface immunoglobulin gamma chains encodes a highly
: conserved transmembrane sequence and a 28-residue intracellular
: domain.";
: Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
: [3]
: SEQUENCE OF 323-366 FROM N.A.
: MEDLINE=82115295; PubMed=6799207;
: Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
: Eisenberg D., Wall R.;
: "Gene segments encoding transmembrane carboxyl termini of
: immunoglobulin gamma chains.";
: Cell 26:19-27(1981).
: [4]
: SEQUENCE OF 1-44 FROM N.A.
: MEDLINE=8222190; PubMed=6283537;
: Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
: "Nucleotide sequences of gene segments encoding membrane domains of
: immunoglobulin gamma chains.";
: Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
: -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
: SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
: GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
: BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
: IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
: SEGMENT OF MU CHAINS.
: -----
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: or send an email to license@isb-sib.ch).
: -----
: EMBL; V00793; CAA241172.1; -
: EMBL; V00793; CAA241173.1; -
: EMBL; V00793; CAA241174.1; -
: PIR; B02159; GIMSM.
: HSSP; P01842; 7FAB.
: MGD; MGI:96446; Igh-4.
: InterPro; IPR003006; Igh_MHC.
: InterPro; IPR003597; Igh-cl.
: Pfam; PF00047; Igh; 3.
: SMART; SM00407; IGcl; 2.
: PROSITE; PS00290; IG_MHC; 1.
: Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
: Alternative splicing; Transmembrane.
: NON_TER 1 1
: DOMAIN 1 97
: CH1.
: FT DOMAIN 1 97
: HINGE.

```

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FT FT DOMAIN 113 219 CH2.
FT FT DOMAIN 220 326 CH3.
FT FT DISULFID 27 82
FT FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT FT DISULFID 140 200
FT FT DISULFID 246 304
FT FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 43.6%; Score 1112; DB 1; Length 326;
Best Local Similarity 61.9%; Pred. No. 8.8e-72;
Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;

2Y 143 AKTTPPSVYPLAPCGDVTGSSVTLGCLVKGYFPEPVTVVWNSGSLSSVHTFPALQSG 202
Db 1 AETTPSVYPLAPGTALKNSMVTLCGLVKGYFPEPVTVVWNSGSLSSVHTFPALQSG 60
2Y 203 LYTMSSSVTPSSVTPSOTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 262
Db 61 LYTLTSSVTPSSVTPSOTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 113
2Y 263 PNLEGGPSVFIFPPNPKDVLMSLTLPKVTVCVVVDVSEDDPDVQISWFVNNVHTAQTOT 322
Db 114 SEVS---SVFIFPPKPKDVLTLTPKVTVCVVVDLSQDDPEVHFSWFVDDVEVHTAQTTP 170
2Y 323 HREDYNTIRVSTLPLOHODMWSGKFEKCKVNNKDLPSPIERTISIKGLVRAPQVYL 382
Db 171 PEEQFNSTFRSVSELPILHQDLWNGRTFRCKVTSAAPSPSEIKTSRPEGTVPHVYTM 230
2Y 383 PPAQQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSFYYSKLN 442
Db 231 SPTKEMTQNEVSTCMVKGYFPDPTDIXEWMNGQPOENYKNTPTMTDGSFYYSKLN 290
2Y 443 MKTSKWEKTSDFSCNVRHEGLKNYLYKKTISRSPGK 478
Db 291 VKKEWQOGNFTFCVLUHEGLHNNHTKSLSHSPGK 326

RESULT 13
CA_RAT
D GCA_RAT STANDARD; PRT; 322 AA.
C P20760;
T 01-FEB-1991 (Rel. 17, Created)
T 01-FEB-1991 (Rel. 17, Last sequence update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
E Ig gamma-2A chain C region.
S Rattus norvegicus (Rat).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
C NCBI_TaxID=10116;
X [1]
N SEQUENCE FROM N.A.
P MEDLINE=89232738; PubMed=3149946;
A Brueggemann M.;
T "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
L Gene 74:473-482(1988).
C -----
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C entities requires a license agreement (see http://www.isb-sib.ch/announce/
C or send an email to license@isb-sib.ch).
C -----
C EMBL; M13804; AAA41376.1; ALT_INIT.
R FIR; PS0019; P50019.
R HSP; P01842; 7FAB.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003597; Ig_c1.
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DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
KW PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 136 196
FT DISULFID 242 300
FT CARBOHYD 172 172
SQ SEQUENCE 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;

Query Match 43.1%; Score 1100; DB 1; Length 322;
Best Local Similarity 60.4%; Pred. No. 6.2e-71;
Matches 203; Conservative 53; Mismatches 66; Indels 14; Gaps 2;

2Y 143 AKTTPPSVYPLAPCGDVTGSSVTLGCLVKGYFPEPVTVVWNSGSLSSVHTFPALQSG 202
Db 1 AETTPSVYPLAPGTALKNSMVTLCGLVKGYFPEPVTVVWNSGSLSSVHTFPALQSG 60
2Y 203 LYTMSSSVTPSSVTPSOTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 262
Db 61 LYTLTSSVTPSSVTPSOTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 107
2Y 263 PNLEGGPSVFIFPPNPKDVLMSLTLPKVTVCVVVDVSEDDPDVQISWFVNNVHTAQTOT 322
Db 108 TGSEVS-SVFIFPPKPKDVLTLTPKVTVCVVVDLSQDDPEVHFSWFVDDVEVHTAQTTP 166
2Y 323 HREDYNTIRVSTLPLOHODMWSGKFEKCKVNNKDLPSPIERTISIKGLVRAPQVYL 382
Db 167 PEKQSNSTLRSVSELPVHVDLWNGRTFRCKVTSAAPSPSEIKTSRPEGTVPHVYTM 226
2Y 383 PPAQQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSFYYSKLN 442
Db 227 APPKEMTQNEVSTCMVKGYFPDPTDIXEWMNGQPOENYKNTPTMTDGSFYYSKLN 286
2Y 443 MKTSKWEKTSDFSCNVRHEGLKNYLYKKTISRSPGK 478
Db 287 VKKEWQOGNFTFCVLUHEGLHNNHTKSLSHSPGK 322

RESULT 14
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gail W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
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QY 322 THREYNSTIRVSTLPTQHQDMGSKFKCKVNNKDLSPERTISKIGLVRAPQVYI 381  
 DB 174 PREQYNSTIRVSVTLVHLQDNLGKEYCKVSNKALPAPTEKTSKAKGQPREPVYT 233  
 QY 382 LPPPAEQLSRDVSITCLVVGFPNGDISVWTSNHTENYKDTAPVLDSDGSIYIYSL 441  
 DB 234 LPPSDELTQVSTCLVVGFPNGDISVWTSNHTENYKDTAPVLDSDGSIYIYSL 293  
 QY 442 NMKTSKWEKTSFSCNVRHEGLNKLKYLKTSRSPGK 478  
 DB 294 TVDKSRWQGNVFCFSVMHEALHNHYTOKSLSPGK 330

RESULT 15

GC RABIT STANDARD; PRT: 323 AA.  
 AC P01870;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma chain C region.  
 JS Oryctolagus cuniculus (rabbit).  
 JC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 JC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 [1]  
 RP SEQUENCE FROM N.A.  
 XX MEDLINE=84030930; PubMed=6313520;  
 XX Bernstein K.E., Alexander C.B., Mage R.G.;  
 XX "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
 XX F-1 haplotype."  
 XX Immunogenetics 18:387-397(1983).  
 [2]  
 RP SEQUENCE OF 1-128.  
 XX MEDLINE=76135469; PubMed=1243651;  
 XX Pratt D.M., Mole L.E.;  
 XX "Sequence studies on the constant region of the Fd sections of rabbit  
 XX immunoglobulin G of different allotype."  
 XX Biochem. J. 151:337-349(1975).  
 [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 XX MEDLINE=83299917; PubMed=6193512;  
 XX Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 XX "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
 XX heavy chain and identification of two genomic C gamma genes."  
 XX Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 [4]  
 RP SEQUENCE OF 132-161.  
 XX MEDLINE=70110015; PubMed=5461106;  
 XX Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 XX "Sequence studies of the Fd section of the heavy chain of rabbit  
 XX immunoglobulin G."  
 XX Biochem. J. 116:249-259(1970).  
 [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 XX Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 XX (in) Killander J. (eds.);  
 XX Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 XX Stockholm (1967).  
 XX -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER.  
 XX 104-THR, AND THE E14 MARKER. 185-THR. REF.3 HAS THE D11 AND E15  
 XX MARKERS AND REF.5 THE E15 MARKER.

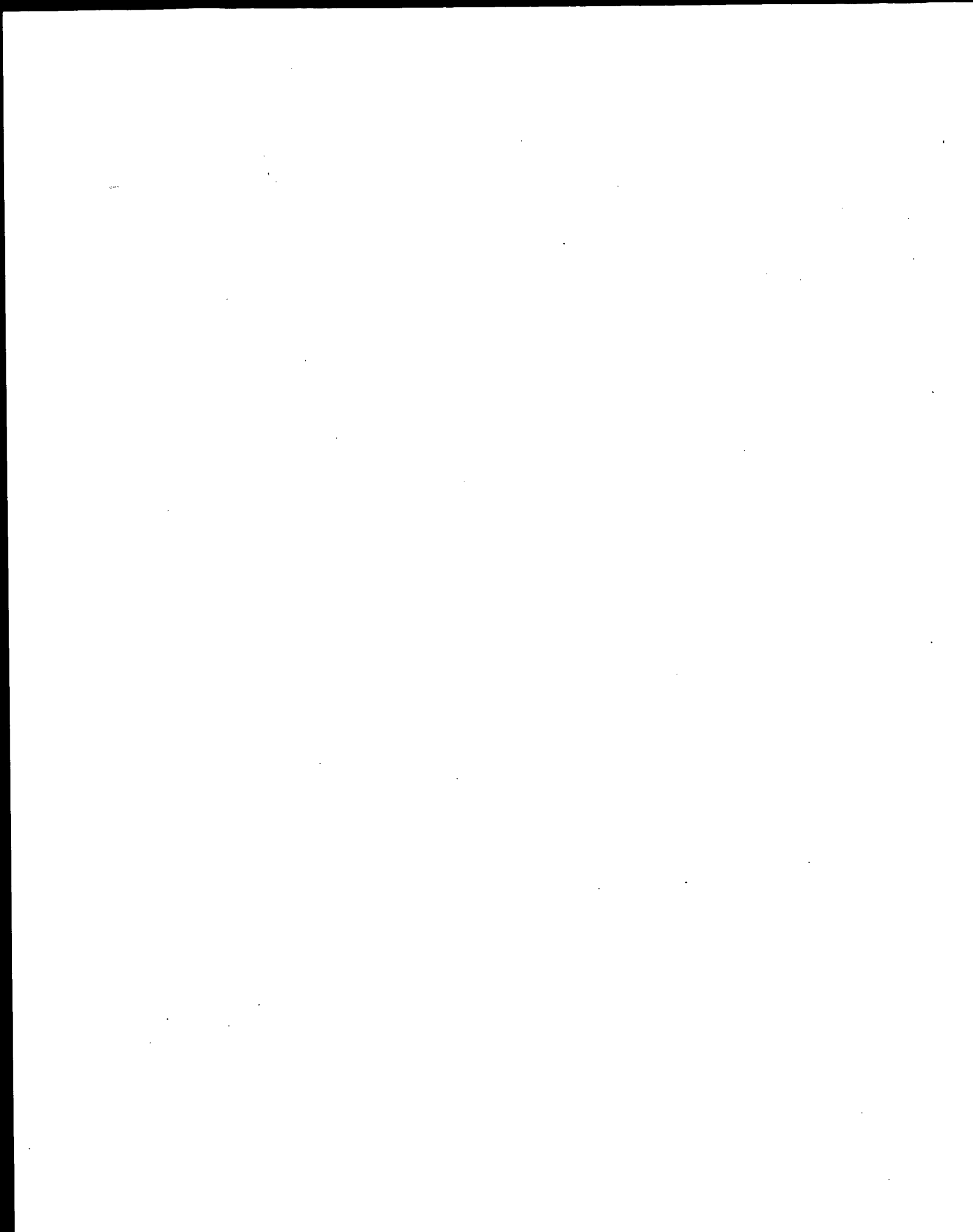
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EMBL; M16426; AAA31289.1; .

DR PIR; A02161; GHRB.  
 DR HSP; P01857; 1FC1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART; SM00407; IgC1; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT VARIANT 104 104 T -> M (IN D11 MARKER).  
 FT VARIANT 185 185 T -> A (IN E15 MARKER).  
 FT CONFLICT 48 48 N -> E (IN REF. 2).  
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).  
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).  
 FT CONFLICT 173 173 N -> D (IN REF. 5).  
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).  
 FT CONFLICT 201 201 N -> D (IN REF. 5).  
 FT CONFLICT 218 218 Q -> E (IN REF. 5).  
 FT CONFLICT 233 233 E -> Q (IN REF. 5).  
 FT CONFLICT 246 246 N -> D (IN REF. 5).  
 FT CONFLICT 256 256 E -> G (IN REF. 5).  
 FT CONFLICT 260 260 N -> D (IN REF. 5).  
 FT CONFLICT 266 266 N -> D (IN REF. 5).  
 FT CONFLICT 280 280 Y -> W (IN REF. 5).  
 FT CONFLICT 284 284 N -> S (IN REF. 5).  
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 42.3%; Score 1080.5; DB 1; Length 323;  
 Best Local Similarity 61.4%; Pred. No. 1.5e-69;  
 Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 4;  
 QY 148 PSVYPLAPCCGDTTSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALLQ-SGLYTM 206  
 DB 6 PSVFPPLAPCCGDTTSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALLQ-SGLYTM 65  
 QY 207 SSVVTPVSTWPSQVTCVAHPASSTTVDKLEPSGPISTINPCPCKECHK--CPAPN 264  
 DB 66 SSVVSTSS--SQPVTCNVAHPATNKTVDKTVAPS-----TCSKPTCPPE 109  
 QY 265 LEGGSPVFIFPNKIDVLMISLTPTKVTGVVDVSDDDPDVQISWFNVVEVHTAQOTHR 324  
 DB 110 LGGSPVFIFPNKIDVLMISLTPTKVTGVVDVSDDDPDVQISWFNVVEVHTAQOTHR 169  
 QY 325 EDYNTIRVSTLPTQHQDMGSKFKCKVNNKDLSPERTISKIGLVRAPQVYI 384  
 DB 170 QQFNSTIRVSTLPTQHQDMGSKFKCKVNNKDLSPERTISKIGLVRAPQVYI 229  
 QY 385 PAEQLSRDVSITCLVVGFPNGDISVWTSNHTENYKDTAPVLDSDGSIYIYSL 444  
 DB 230 PREELSSRSVSLTCMNGFYPSDISVWEKNGKAEDNKTTPAVLDSDGSIYIYSL 289  
 QY 445 TSKWEKTSFSCNVRHEGLNKLKYLKTSRSPGK 478  
 DB 290 TSEWQRGDVFTCSVMHEALHNHYTOKSLSPGK 323

Search completed: June 18, 2003, 16:42:31  
 Job time : 20.4691 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 34.9101 Seconds  
(without alignments)  
1316.302 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVLGLLFLVTFPSCVLSQ.....RHEGLKNYKKTISRSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2067	81.0	474	1 G2MS11	Ig gamma-2b chain
2	2024.5	79.3	475	2 S01321	Ig gamma-2b chain
3	1797	70.4	405	1 G2MSBM	Ig gamma-2b chain
4	1739	68.1	446	2 S40295	Ig gamma-2a chain
5	1727.5	67.7	469	2 S37483	Ig gamma-2a chain
6	1485.5	58.2	444	2 PC4436	monoclonal antibody
7	1456.5	57.1	472	2 S31459	Ig gamma-1 chain
8	1427.5	55.9	470	2 S22080	Ig heavy chain pre
9	1419	55.6	330	1 G2MSA	Ig gamma-2a chain
10	1414	55.4	339	1 G2MSAM	Ig gamma-2a chain
11	1385.5	54.3	335	1 G2MSAB	Ig gamma-2a chain
12	1326.5	52.0	333	2 PS0018	Ig gamma-2a chain
13	1302.5	47.1	329	2 S00847	Ig gamma-2c chain
14	1170	45.8	329	1 G3MSC	Ig gamma-3 chain C
15	1159	45.4	338	1 G3MSW	Ig gamma-3 chain C
16	1150	45.1	324	1 G1MS	Ig gamma-1 chain C
17	1145	44.9	333	1 G1MSM	Ig gamma-1 chain C
18	1112	43.6	326	2 PS0017	Ig gamma-1 chain C
19	1100	43.1	322	2 PS0019	Ig gamma-1 chain C
20	1087	42.6	330	1 GHU	Ig gamma-2a chain
21	1080.5	42.3	323	1 GHRB	Ig gamma-1 chain C
22	1080.5	42.3	329	1 G2GP	Ig gamma chain C r
23	1072.5	42.0	377	2 A60764	Ig gamma-2 chain C
24	1072.5	42.0	377	2 A23511	Ig gamma-3 chain C
25	1059	41.5	326	2 G2HU	Ig gamma-2 chain C
26	1058	41.5	328	2 I47159	Ig gamma-2a chain
27	1054.5	41.3	327	1 G4HU	Ig gamma-4 chain C
28	1053	41.3	374	2 S69339	Ig heavy chain V r
29	1049	41.1	328	2 I47160	Ig gamma 2b chain

ALIGNMENTS

RESULT 1

G2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000

C:Accession: S25057; A26235; A26232; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25057

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>

A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.

Nature 283, 786-789, 1980

A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro

A:Reference number: A02157; MUID:80120716; PMID:6766534

A:Contents: a allele

A:Accession: A02157

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>

A:Cross-references: GB:J00461

A>Note: the sequence was determined from the germline gene

R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b

A:Reference number: A26235; MUID:80081501; PMID:117548

A:Contents: MPC 11

A:Accession: A26235

A:Molecule type: mRNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>

A>Note: Lys-474 is probably removed posttranslationally

R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.

Science 206, 1303-1306, 1979

A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno

A:Reference number: A26232; MUID:80081502; PMID:117549

A:Accession: A26232

A:Molecule type: DNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>

R:Ollo, R.; Rougeon, F.

Nature 296, 761-763, 1982

A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g

A:Reference number: A26233; MUID:82173203; PMID:6803173

A:Accession: A26233

A:Contents: b allele

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL

A:Cross-references: GB:J00461

R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah

J. Biol. Chem. 269, 12345-12350, 1994

Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
Reference number: A53598; MUID:94216359; PMID:7512967

Accession: A53598  
Status: preliminary  
Molecule type: protein  
Residues: 234-251 <KIM>  
Comment: The a allele sequence is shown.

Genetics:  
Introns: 138/1; 236/1; 258/1; 368/1  
Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) and two heavy (h) chains, each with two variable and three constant domains. The chains are linked by disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers. Immunoglobulin C region; immunoglobulin homology  
Superfamily: immunoglobulin C region; immunoglobulin homology  
Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology  
157-222/Domain: immunoglobulin homology <IM1>  
236-257/Region: hinge  
281-350/Domain: immunoglobulin homology <IM2>  
387-434/Domain: immunoglobulin homology <IM3>  
152/Disulfide bonds: interchain (to light chain) #status predicted  
164-220,288-348,394-452/Disulfide bonds: #status predicted  
247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
324/Binding site: carbohydrate (Asn) #status predicted

Query Match	81.0%;	Score	2067;	DB 1;	Length	474;
Best Local Similarity	83.8%;	Pred. No.	1.1e-117;			
Matches	389;	Conservative	29;	Mismatches	38;	Indels
						Gaps
						4;

17	VLSQVQLKQSGPGLVQPQSGSLTCTVSGFSLTSYGVHWRQSPGKGLWLGVIWSG	GD-75
17	VHSEYQLQSGPELVNPGASVKMSKASGYITFTYVHWKQKPGQGLEWIGYINPNKDG	76
76	TDYNAAFISRLSISKDNKSKQLFFKMNSLRATDTAIYYCARNRGDIYYDYFYAMDYWGQ	135
77	TFNEKFKGKATLSDKSNAYMELSLTSEDSAVYFCARD----	YDYNW-FAYWGQ 130
136	TSVTSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTF	195
131	TLVTVAATTPPSVYPLAPGCGDTTGSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTL	190
196	-PALLOSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTVDKLEPSGPISTINPCPPC	254
191	SOALLQSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTVDKLEPSGPISTINPCPPC	250
255	KECHKCAPNLEGGSPVFPPNPKDVLMSLTLPKVTVCVVDVSEDDPDVQISWVFNVE	314
251	KECHKCAPNLEGGSPVFPPNPKDVLMSLTLPKVTVCVVDVSEDDPDVQISWVFNVE	310
315	VHTAQQTTHREDYNSTIRVSTPLTQHDWMSGKFKCKVNNKDLPSPIERTISKIGLV	374
311	VHTAQQTTHREDYNSTIRVSTPLTQHDWMSGKFKCKVNNKDLPSPIERTISKIGLV	370
375	RAPQVYILPPAPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS	434
371	RAPQVYILPPAPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS	430
435	YTIYSKLNKMTSKWEKTSDFSCNVRHEGLKNYLLKKTISRSPCK	478
431	YFIYSKLNKMTSKWEKTSDFSCNVRHEGLKNYLLKKTISRSPCK	474

RESULT 2

I gamma-2b chain precursor - mouse  
Species: Mus musculus (house mouse)  
Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
Accession: S01321  
R: de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
r. J. Biochem. 176, 287-295, 1988  
Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
Reference number: S01320; MUID:88329081; PMID:3138116  
Accession: S01321  
Molecule type: mRNA  
Residues: 1-475 <DE1>  
Cross-references: EMBL:X13188; NID:g51780; PIDN:CRAA31580.1; PID:g51781

A: Note: this sequence was determined from the differentiated gene  
C: Superfamily: immunoglobulin C region; immunoglobulin homology  
C: Keywords: immunoglobulin  
F: 1-19/Domain: signal sequence #status predicted <SIG>  
F: 20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F: 159-223/Domain: immunoglobulin homology <IMW>

Query Match 79.3%; Score 2024.5; DB 2; Length 475;  
Best Local Similarity 82.3%; Pred. No. 4.2e-115;  
Matches 381; Conservative 30; Mismatches 47; Indels 5; Gaps 2;

QY	17	VLSQVQLKQSGPGLVQPQSGSLTCTVSGFSLTSYGVHWRQSPGKGLWLGVIWSG	GD-75
DB	17	VQSQVQLQSGAELARPGASVKLSKASGYITLTSIGISWVKQRTQGLEWIGEYIPGSGN	76
QY	76	TDYNAAFISRLSISKDNKSKQLFFKMNSLRATDTAIYYCARNRGDIYYDYFYAMDYWGQ	135
DB	77	SYFNEKFKGKATLTVDKSSSTAYLHLSLTSEDSAVYFCAGPRQVGLLPF----	GYWGQ 132
QY	136	TSVTSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTF	195
DB	133	TLVTASAAKTTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTF	192
QY	196	PALLOSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTVDKLEPSGPISTINPCPPCK	255
DB	193	PALLOSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTVDKLEPSGPISTINPCPPCK	252
QY	256	ECHKCAPNLEGGSPVFPPNPKDVLMSLTLPKVTVCVVDVSEDDPDVQISWVFNVE	315
DB	253	ECHKCAPNLEGGSPVFPPNPKDVLMSLTLPKVTVCVVDVSEDDPDVQISWVFNVE	312
QY	316	HTAQQTTHREDYNSTIRVSTPLTQHDWMSGKFKCKVNNKDLPSPIERTISKIGLV	375
DB	313	LTAQQTTHREDYNSTIRVSTPLTQHDWMSGKFKCKVNNKDLPSPIERTISKIGLV	372
QY	376	APQVYILPPAPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS	435
DB	373	APQVYILPPAPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS	432
QY	436	YTIYSKLNKMTSKWEKTSDFSCNVRHEGLKNYLLKKTISRSPCK	478
DB	433	YFIYSKLNKMTSKWEKTSDFSCNVRHEGLKNYLLKKTISRSPCK	475

RESULT 3  
G2B5M

Ig gamma-2b chain C region, membrane-bound form - mouse  
Species: Mus musculus (house mouse)  
C: Date: 17-Dec-1982 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999  
C: Accession: C02154; A02158; B02157  
R: Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.  
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982  
A: Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin  
A: Reference number: A02154; MUID:82222190; PMID:6283537

A: Accession: C02154  
A: Molecule type: DNA  
A: Residues: 335-405 <YAM>  
A: Cross-references: GB:J00462  
R: Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wa  
Cell 26, 19-27, 1981  
A: Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma  
A: Reference number: A02158; MUID:82115295; PMID:6799207  
A: Accession: A02158  
A: Molecule type: DNA  
A: Residues: 335-378 <ROG>  
A: Note: the translation of the first exon of the membrane-bound segment is given  
R: Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A: Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro  
A: Reference number: A02157; MUID:80120716; PMID:6766534  
A: Contents: a allele.  
A: Accession: B02157  
A: Molecule type: DNA

Accession: S40295  
 A: Molecule type: protein  
 A: Residues: 1-446 <KLE>  
 A: Geneticks:  
 A: Map position: 12  
 A: Superfamily: immunoglobulin C region; immunoglobulin homology  
 A: Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
 A: I-446/Product: Ig gamma-2a chain #status experimental <MAT>  
 A: V-1-117/Domain: V-D-J region <VDJ>  
 A: I18-446/Domain: C region <CHR>  
 A: I18-214/Domain: C1 region <CH1>  
 A: I215-230/Region: hinge  
 A: I231-340/Domain: C2 region <CH2>  
 A: I341-446/Domain: C3 region <CH3>  
 A: I360-427/Domain: immunoglobulin homology <IMM>  
 A: I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 A: I22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
 A: I132/Disulfide bonds: interchain (to light chain) #status predicted  
 A: I224,227,229/Disulfide bonds: interchain #status predicted

[illegible]



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C:Accession: PS0018; B25941  
R:Brueggemann, M.  
Gene 74, 473-482, 1988  
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.  
A:Reference number: PS0017; MUID:89232738; PMID:3149946  
A:Accession: PS0018  
A:Molecule type: DNA  
A:Residues: 1-333 <BRU>  
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986  
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody  
A:Reference number: A25941; MUID:86287397; PMID:3016742  
A:Accession: B25941  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 227-333 <BR2>  
C:Genetics:  
A:Introns: 96/1; 117/1; 227/1  
C:Superfamily: immunoglobulin c region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-82/Domain: immunoglobulin homology <IMM>  
Query Match 52.0%; Score 1326.5; DB 2; Length 333;  
Best Local Similarity 73.6%; Pred. No. 4e-73;  
Matches 248; Conservative 34; Mismatches 50; Indels 5; Gaps 3;  
QY 143 AKTTPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTNWNSGLSSSVHTFPALQSG 202  
Db 1 ARTTAPSVYPLVPCGCGTSGSLVTLGCLVKGYPPEVTVTNWNSGALSSDVHTFPALQSG 60  
QY 203 LYTMSSSVTPSPSTWPSQTVTCVAHPASSTVVDKLE-PSGPISITINCPCKECKCP 261  
Db 61 LYTLNSSVT--SSTWPSQTVTCVAHPASSTVVDKLE-PSGPISITINCPCKECKCP 116  
QY 262 APNLEGGPSVFIPPNKIDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 321  
Db 117 VPELLGGPSVFIPPNKIDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 176  
QY 322 THREDYNTIRVSTPLTQHDWMSGKFEKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 381  
Db 177 PREEQYNSFTFRVYSLPIQHODWMSGKFEKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 236  
QY 382 LPPAEQLSRKDVSLTCLVGVNPGDISVEWTSNGHTENYKDTAPVLDSDGSYFIYSKL 441  
Db 237 MGPTTEQTEQVSLTCLTSGFLVNDIGVWTSNGHIEKNYKNTPEVMDSDGSFFMYSKL 296  
QY 442 NMKTSKWEKTDSCFNVRHEGLKNYLLKKTISRSPGK 478  
Db 297 NVRSRWDSPRAFCVSVVHEGLNHHVKSISRPGK 333  
RESULT 13  
S00847  
Ig gamma-2c chain C region - rat (fragment)  
Species: Rattus norvegicus (Norway rat)  
Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 23-Jul-1999  
Accession: S00847  
Eur. J. Immunol. 18, 317-319, 1988  
A:Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: ext  
A:Reference number: S00847; MUID:88166903; PMID:3127222  
A:Accession: S00847  
A:Molecule type: mRNA  
A:Residues: 1-329 <BRU>  
Cross-references: EMBL:X07189; NID:57602; PID:CAA30169.1; PID:g663228  
Superfamily: immunoglobulin C region; immunoglobulin homology  
Keywords: immunoglobulin  
F:20-84/Domain: immunoglobulin homology <IMM>  
Query Match 47.1%; Score 1202.5; DB 2; Length 329;  
Best Local Similarity 68.2%; Pred. No. 1.2e-65;  
Matches 229; Conservative 35; Mismatches 65; Indels 7; Gaps 4;

QY 143 AKTTPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTNWNSGLSSSVHTFPALQSG 202  
Db 1 ARTTAPSVYPLVPCGCGTSGSLVTLGCLVKGYPPEVTVTNWNSGALSSDVHTFPALQSG 60  
QY 203 LYTMSSSVTPSPSTWPSQTVTCVAHPASSTVVDKLEPSGPISITINCPCKECKCPA 262  
Db 61 LYTLSSSVTPSPSTWPSQTVTCVAHPASSTVVDKLEPSGPISITINCPCKECKCPA 114  
QY 263 PNLEGGPSVFIPPNKIDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 322  
Db 115 DNL-GRPSVFIPPNKIDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOT 173  
QY 323 HREDYNTIRVSTPLTQHDWMSGKFEKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 382  
Db 174 HEQLNGTFRVSTPLTQHDWMSGKFEKCKVNNKDLPSPIERTISKIKGLVRAPOVYIL 233  
QY 383 PPAEQLSRKDVSLTCLVGVNPGDISVEWTSNGHTENYKDTAPVLDSDGSYFIYSKL 442  
Db 234 PPREQMSKNKVSILTCMTSFPASISVEWERNGELEQDKNTLPVLDSDGSYFIYSKL 293  
QY 443 MKTSKWEKTDSCFNVRHEGLKNYLLKKTISRSPGK 478  
Db 294 VDTDSWNRGDIYTCVSVVHEALNHHHTQKNLSRSPGK 329  
RESULT 14  
G3MSC  
Ig gamma-3 chain C region, secreted form - mouse  
Species: Mus musculus (house mouse)  
C:Date: 17-Mar-1987 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999  
C:Accession: B02156  
R:Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Bl  
EMBO J. 3, 2041-2046, 1984  
A:Title: Structure analysis of the murine IgG3 constant region gene.  
A:Reference number: A02156; MUID:85027161; PMID:6092053  
A:Accession: B02156  
A:Molecule type: DNA  
A:Residues: 1-329 <WEL>  
A:Cross-references: GB:J00451  
A:Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Introns: 97/1; 113/1; 223/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl  
F:19-83/Domain: immunoglobulin homology <IMI>  
F:97-112/Region: hinge  
F:136-205/Domain: immunoglobulin homology <IM2>  
F:242-309/Domain: immunoglobulin homology <IM3>  
F:179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 45.8%; Score 1170; DB 1; Length 329;  
Best Local Similarity 66.2%; Pred. No. 1.1e-63;  
Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1;  
QY 145 TTPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTNWNSGLSSSVHTFPALQSGLY 204  
Db 2 TTPSVYPLVPCGCGTSGSLVTLGCLVKGYPPEVTVTNWNSGALSSDVHTFPALQSGFY 61  
QY 205 TMSSSVTPSPSTWPSQTVTCVAHPASSTVVDKLEPSGPISITINCPCKECKCPAPN 264  
Db 62 SLSLVTVPSPSTWPSQTVTCVNAHPASSTVVDKLEPSGPISITINCPCKECKCPAPN 115  
QY 265 LEGGPSVFIPPNKIDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOTHR 324  
Db 116 ILGSPSVFIPPNKIDVLMISLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQOTPRE 175  
QY 325 EDYNTIRVSTPLTQHDWMSGKFEKCKVNNKDLPSPIERTISKIKGLVRAPOVYILPP 384  
Db 176 AQYNSTFRVYSLPIQHODWMSGKFEKCKVNNKALPAIERTISKIKGRAQTPQVYITPP 235  
QY 385 PAEQLSRKDVSLTCLVGVNPGDISVEWTSNGHTENYKDTAPVLDSDGSYFIYSKLNMK 444





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 56.3933 Seconds  
(without alignments)  
2164.388 Million cell updates/sec

Title: US-09-770-916-2  
Perfect score: 2552  
Sequence: 1 MAVLGLFCLVFPSCVLSQ.....RHEGLKNYKLTISRSPGK 478

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1156168 seqs, 255349102 residues

Total number of hits satisfying chosen parameters: 1156168

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	1666.5	65.3	469	6	US-10-429-662-10	Sequence 10, Appl
2	1666.5	65.3	469	6	US-10-429-660-10	Sequence 12, Appl
3	1643	64.4	468	1	PCT-US02-02373-12	Sequence 10, Appl
4	1565.5	61.3	446	5	US-09-618-380A-7	Sequence 7, Appl
5	1497.5	58.7	462	1	PCT-US02-34420A-23	Sequence 23, Appl
6	1497.5	58.7	462	1	PCT-US02-35333A-23	Sequence 23, Appl
7	1497.5	58.7	462	6	US-10-286-132A-23	Sequence 23, Appl
8	1497.5	58.7	462	6	US-10-281-479A-23	Sequence 23, Appl
9	1497.5	58.7	464	6	US-10-275-180A-23	Sequence 23, Appl
10	1472	57.7	464	6	US-10-384-933-9	Sequence 9, Appl
11	1462.5	57.3	361	6	US-10-272-899A-82	Sequence 82, Appl
12	1457	57.1	474	1	PCT-US02-36107-14	Sequence 14, Appl
13	1457	57.1	474	6	US-10-292-088-14	Sequence 14, Appl
14	1452.5	56.9	361	6	US-10-272-899A-80	Sequence 80, Appl
15	1451	56.9	466	1	PCT-US02-36107-70	Sequence 70, Appl
16	1451	56.9	466	6	US-10-292-088-70	Sequence 70, Appl
17	1449	56.8	464	1	PCT-US02-36107-22	Sequence 22, Appl
18	1449	56.8	464	6	US-10-292-088-22	Sequence 22, Appl
19	1449	56.8	466	1	PCT-US02-36107-86	Sequence 86, Appl
20	1449	56.8	466	6	US-10-292-088-86	Sequence 86, Appl
21	1448	56.7	466	1	PCT-US02-36107-30	Sequence 30, Appl
22	1448	56.7	466	6	US-10-292-088-30	Sequence 30, Appl
23	1446	56.7	451	1	PCT-US03-13054-4	Sequence 4, Appl
24	1446	56.7	451	6	US-10-423-299-4	Sequence 4, Appl
25	1445.5	56.6	469	1	PCT-US03-10154-72	Sequence 72, Appl
26	1445.5	56.6	469	6	US-10-404-724-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-10-429-662-10  
; Sequence 10, Application US/10429662  
; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir  
; TITLE OF INVENTION: Compositions For Nucleic Acid Delivery  
; FILE REFERENCE: 2537.000010  
; CURRENT APPLICATION NUMBER: US/10/429,662  
; CURRENT FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-429-662-10

Query Match 65.3%; Score 1666.5; DB 6; Length 469;  
Best Local Similarity 66.2%; Pred. No. 1e-99;  
Matches 317; Conservative 62; Mismatches 89; Indels 11; Gaps 5;

QY	1	MAVLGLFCLVFPSCVLSQVQLKQSGPGLVPSQSLISITCTVSGFSLTSGYGVHWRQSP	60
DB	1	MAVLGLFCLVFPSCVLSQVHLKESGPGVAPQSLSITCTVSGFSLTSGYGVHWRQPP	60
QY	61	KGKLEWLGVIWGGDTDYNAAFISRLSISKNSKSOLEFFKMSLRATDTAIYYCARNRGD	120
DB	61	KGKLEWLGVIWGGDTDYNSALMSRLSINKNSKSOVFLKMSLQADDTAIYYCARFRA	120
QY	121	IYDFTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPGCGDTTGGSSVTLGCLVKGYPPEV	180
DB	121	SYVD--YAVDYWGQGTSTVTVSS--TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV	177
QY	181	VTVNWSGSLSSSVHTFPALIQ--SGLYTMSSSVTVPSSTWPSQTVCVAHPASSTVDDKL	239
DB	178	VSNNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSTWPSQTVCVAHPASSTVDDKV	237
QY	240	ESGPSITINCPCKCKECHKCAPNLEGGPSVFIFPPNKKIVMLISLTPKVCVVVDVSE	299
DB	238	EPKSCDKT--HTCPP-----CPAPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSH	290
QY	300	DDPDVQISWVNNVHTAOTQTHREDYNSIRVYSTPIQHODMWSGKEFKCKYNNKDL	359
DB	291	EDPEVKFNWYVDGVGVHNAKTPREEQNSTYRVVSLTVLHDLWNGKEYCKYCKYNNKAL	350
QY	360	PSPIERTISKIQLVRAPQVYILPPPAQLSRKDYSLTCLVGVNPGDTSVETWSNGHTE	419
DB	351	PAPIETKISKAKQPREQVYTLPPSRDELKQVSLTCLVKGFPYSLDIAVWESNGOPE	410



Query Match 61.3%; Score 1565.5; DB 5; Length 446;  
Best Local Similarity 64.1%; Pred. No. 3.2e-93;  
Matches 295; Conservative 63; Mismatches 87; Indels 15; Gaps 4;

QY 20 QVQLKSGFGLVQPSQSLSITCTVSGFSLTSYGVHVRQSPGKGLWGLVWISGGDDTDXN 79  
Db 1 QVQLQSGFGLVQPSQSLSITCTVSGFSLTSYGVHVRQSPGKGLWGLVWISGGSTEYN 60

QY 80 APTISRLTSKDNKSKQSLFFKMNLSRATDAIYYCARNRGGDIYYDFTYAMDYWGQGTSTV 139  
Db 61 AAFISRLTSKDNKSKQSLFFKMNLSRATDAIYYCARNRGGDIYYDFTYAMDYWGQGTSTV 113

QY 140 VSAKATTPSPVPLAPGCGDTTSSVTGLCLVKGYPPEVTVWNSGSSSVSHHTFPALL 199  
Db 114 VSAKATTPSPVPLAPGCGDTTSSVTGLCLVKGYPPEVTVWNSGSSSVSHHTFPALL 199

QY 200 Q-SGLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVDKLEPSGPISTINPCPKCKECH 258  
Db 174 QSGSLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVDKLEPSGPISTINPCPKCKECH 227

QY 259 KCPAPNLEGGPSVFIPPPNKKVLMISLTPKVTCTVVVDYSEDDPDVQISGFVNNEVHTA 318  
Db 228 -CPAPNLEGGPSVFIPPPNKKVLMISLTPKVTCTVVVDYSEDDPDVQISGFVNNEVHTA 286

QY 319 QPTQTHREDYNSIRVSTLPIQHDQMSKCKCKVNNKDLPSPIERTISKIKGLVRAPQ 378  
Db 287 KTKPREQYNSIRVSTLPIQHDQMSKCKCKVNNKDLPSPIERTISKIKGLVRAPQ 346

QY 379 VYLPPAPQLSRKDVSLTCLVVGPNPGDISVWTSNGHTENYKDTAPVLDSDGSFYFI 438  
Db 347 VYLPPAPQLSRKDVSLTCLVVGPNPGDISVWTSNGHTENYKDTAPVLDSDGSFYFI 406

QY 439 SKLNKMTSKWEKTDSCFNVRHEGLKNYLLKKTISRSPGK 478  
Db 407 SKLTVDKRWQGNVFSQVSMHEALHNYTKQSLSLSPGK 446

RESULT 5  
PCT-US02-34420A-23  
; Sequence 23, Application PC/TUS0234420A  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: Oshumi, Jun  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS FACTOR-  
; FILE REFERENCE: 21085.0029P3  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US02/34420A  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: 60/391,478  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 23  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct  
PCT-US02-34420A-23

Query Match 58.7%; Score 1497.5; DB 1; Length 462;  
Best Local Similarity 61.1%; Pred. No. 8.1e-89;  
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;

Best Local Similarity 61.1%; Pred. No. 8.1e-89;  
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;

QY 4 LGLLFCVLTTPSCVLSQVQLKQSGPGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGK 63  
Db 5 LSLIF-LVLVLKGVQCEVLMVSGGLVLPKGGSLKLSAASGFTFSYVMSVWRQTPEKR 63

QY 64 LEWLGVTWGGD-TDYNAAFISRLTSKDNKSKQSLFFKMNLSRATDAIYYCARNRGGDIY 122  
Db 64 LEWATISSGGSYIYPPDSVKGRTTISRDNKNTLYLQMSLSRSEDAMYYCAR-RG--- 119

QY 123 YDFTYAMDYWGQGTSTVTSVSAKATTPSPVPLAPGCGDTTSSVTGLCLVKGYPPEVTVT 182  
Db 120 -DSMITTDYWGQGTSTVTSVSAKATTPSPVPLAPGCGDTTSSVTGLCLVKGYPPEVTVT 178

QY 183 WNSGSLSSSVHTTPALLQSGLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVDKLEPS 242  
Db 179 WNSGSLSSSVHTTPALLQSGLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVDKLEPS 237

QY 243 GPISTINPCPKCKECHKCAPNLEGGPSVFIPPPNKKVLMISLTPKVTCTVVVDYSEDD 302  
Db 238 -----RDC-GCPC-ICTVPEVS--SVFIFPPKPKDVLITLTTPKVTCTVVVDYSEDD 286

QY 303 DVOISFVNNEVHTAQTOHREDYNSIRVSTLPIQHDQMSKCKCKVNNKDLPS 362  
Db 287 EVQSFVDDVHTAQTOHREDYNSIRVSTLPIQHDQMSKCKCKVNNKDLPS 346

QY 363 IERTISKIKGLVRAPQVYIILPPAPQLSRKDVSLTCLVVGPNPGDISVWTSNGHTENY 422  
Db 347 IERTISKIKGLVRAPQVYIILPPAPQLSRKDVSLTCLVVGPNPGDISVWTSNGHTENY 406

QY 423 KDTAPVLDSDGSFYFIYKLNKMTSKWEKTDSCFNVRHEGLKNYLLKKTISRSPGK 478  
Db 407 KNTQPIMDTDGYSFYVSKLVNQRNWEAGNTCTCVLHEGLHNNHTEKSLSHSPGK 462

RESULT 6  
PCT-US02-35333A-23  
; Sequence 23, Application PC/TUS0235333A  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: LoBuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
; FILE REFERENCE: 21085.0029P2  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: PCT/US02/35333A  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 23  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
; OTHER INFORMATION: Synthetic Construct  
PCT-US02-35333A-23

Query Match 58.7%; Score 1497.5; DB 1; Length 462;  
Best Local Similarity 61.1%; Pred. No. 8.1e-89;  
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;

[illegible]

## RESULT 7

3-10-286-132A-23  
 Sequence 23, Application US/10286132A  
 GENERAL INFORMATION:  
 APPLICANT: Zhou, Tong  
 APPLICANT: Kimberly, Robert P.  
 APPLICANT: Koopman, William J.  
 APPLICANT: LoBuglio, Albert S.  
 APPLICANT: Buchsbaum, Donald J.  
 TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
 TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
 FILE REFERENCE: 21085.002907  
 CURRENT APPLICATION NUMBER: US/10/286, 132A  
 CURRENT FILING DATE: 2003-01-22  
 PRIOR APPLICATION NUMBER: US 60/346,402  
 PRIOR FILING DATE: 2001-11-01  
 PRIOR APPLICATION NUMBER: PCT/US01/14151  
 PRIOR FILING DATE: 2001-05-02  
 PRIOR APPLICATION NUMBER: US 60/201,344  
 PRIOR FILING DATE: 2000-05-02  
 NUMBER OF SEQ ID NOS: 102  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 23  
 LENGTH: 462  
 TYPE: PRT  
 ORGANISM: artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Cons  
 3-10-286-132A-23

## RESULT 8

```

US-10-281-479A-23
; Sequence 23, Application US/10281479A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
US-10-281-479A-23

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411 TOPIMNTNGSYFVYSKLVNQKSNWEAGNTFTCSVLHGLHNHTEKSLSHSPGK 464

RESULT 11

Sequence 82, Application US/10272899A

GENERAL INFORMATION:

APPLICANT: O'Keefe, Theresa L.

APPLICANT: Healy, Judith Jacques

APPLICANT: Newman, Walter

APPLICANT: Ponath, Paul

APPLICANT: Bruce Keyt

TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,

TITLE OF INVENTION: MONOCYCLONAL ANTIBODIES TO CD40

TITLE OF INVENTION: USE THEREFOR

FILE REFERENCE: MP101-244P2RM

CURRENT APPLICATION NUMBER: US/10/272,899A

CURRENT FILING DATE: 2002-10-17

PRIOR APPLICATION NUMBER: 60/350,166

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: 60/392,364

PRIOR FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 82

LENGTH: 361

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: immunoglobulin cassette protein sequence

OTHER INFORMATION: Leader-Mu\_WT\_60

3-10-272-899A-82

Query Match 57.3%; Score 1462.5; DB 6; Length 361;

Best Local Similarity 59.8%; Pred. No. 1.1e-86;

Matches 286; Conservative 35; Mismatches 40; Indels 117; Gaps 2;

1 MAVLGLLFCLVTLPCVLSRL----- 21

1 MAVLGLLFCLVTLPCVLSRL----- 21

61 GKGLEWLVGIVSGGDTDYNAAFISRLISKDNKSKQLFFKMSLRATDTAIYYCARNRGD 120

22 ----- 21

121 IYDFTYAMDWYQGTSTVSSAKTTPPSVYPLAPGCGDTTSSVTLGCLVKGYPPEVY 180

22 ----- 21

181 VTWNSGSLSSVHTFPALQSGLYTMSSSVTPSPSTVPSQVTSVAHPASSTVVDKLE 240

65 LTWNSGSLSSVHTFPALQSGLYTMSSSVTPSPSTVPSQVTSVAHPASSTVVDKLE 124

241 PSGTISTINPCPPCKECHKCAPNLEGGPSVFIFPPNIDKLMISLTPKVTVCVVVDVSD 300

125 PRVPI-TQNPCPLKECPCAAPDLGLGSPVFIFPPNIDKLMISLTPKVTVCVVVDVSD 183

301 DPVQISWVFNVEVHTAQTHREDYNSTIRVSTLPIQHDQDMSGKFEKCKVNNKDL 360

184 DPVQISWVFNVEVHTAQTHREDYNSTIRVSTLPIQHDQDMSGKFEKCKVNNKDL 243

361 SPIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVWTSNGHTE 420

244 SPIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVWTSNGHTE 303

421 NYKDTAPVLDSDGSGFYISKLNKMTSKWEKTSFSCNVRHEGLNKLTKTSRSPGK 478

304 NYKDTAPVLDSDGSGFYISKLNKMTSKWEKTSFSCNVRHEGLNKLTKTSRSPGK 361

RESULT 12

CT-US02-36107-14

Sequence 14, Application PC/TUS0236107

GENERAL INFORMATION:

APPLICANT: ABGENIX, INC.

APPLICANT: PFIZER PRODUCTS INC.

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 PCT

CURRENT APPLICATION NUMBER: PCT/US02/36107

CURRENT FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 474

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US02-36107-14

Query Match 57.1%; Score 1457; DB 1; Length 474;

Best Local Similarity 58.6%; Pred. No. 3.4e-86;

Matches 280; Conservative 72; Mismatches 104; Indels 22; Gaps 7;

QY 10 LVTFPSCVLSQVQLKQSGPGLVPSQSLITCTVSGFSLTSGVHVRQSPGKLEWLV 69

DB 10 LVALLRGVQCQQLVESGGVGVVQPGSRSLRLCAASGFTFSSYGMHVRQAPCKGLEWAV 69

QY 70 IWSGGDTDYNAAFI-SRLISKDNKSKQLFFKMSLRATDTAIYYCAR-----NRGDI 121

DB 70 ISNDGNKYHADSVMGRFTISRDNRSRTLYLQMSLRADTAIYYCARRGMGSGSRGDI 129

QY 122 YDFTYAMDWYQGTSTVSSAKTTPPSVYPLAPGCGDTTSGVTLGCLVKGYPPEVY 181

DB 130 YY-YVGLDVGQGTSTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKGYPPEVY 187

QY 182 TWNSGSLSSVHTFPALQ-SGLYTMSSSVTPSPSTVPSQVTSVAHPASSTVVDKLE 240

DB 188 SWSGALTSGVHTFPAVLQSSGLYSLSSVTPSPSTVPSQVTSVAHPASSTVVDKLE 247

QY 241 PSGTISTINPCPPCKECHKCAPNLEGGPSVFIFPPNIDKLMISLTPKVTVCVVVDVSD 300

DB 248 -----RKC--CVCPCPCAPPV-AGPSVFLFPKPKDMLISTPTVEVTVVDSHE 296

QY 301 DPVQISWVFNVEVHTAQTHREDYNSTIRVSTLPIQHDQDMSGKFEKCKVNNKDL 360

DB 297 DEVOFNWVVDGVEVHNAKTPREEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLP 356

QY 361 SPIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVWTSNGHTE 420

DB 357 APIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVWTSNGHTE 416

QY 421 NYKDTAPVLDSDGSGFYISKLNKMTSKWEKTSFSCNVRHEGLNKLTKTSRSPGK 478

DB 417 NYKTPPMLDSDGSGFYISKLNKMTSKWEKTSFSCNVRHEGLNKLTKTSRSPGK 474

RESULT 13

US-10-292-088-14

Sequence 14, Application US/10292088

GENERAL INFORMATION:

APPLICANT: BEDIAN, VAHE

APPLICANT: GLADUE, RONALD P.

APPLICANT: CORVALAN, JOSE

APPLICANT: JIA, XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 US

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 474

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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-088-14

Query Match 57.1%; Score 1457; DB 6; Length 474;
Best Local Similarity 58.6%; Pred. No. 3.4e-86;
Matches 280; Conservative 72; Mismatches 104; Indels 22; Gaps 7;

QY 10 LVTFPSCVLISOVLQSGPCLVOPSOGLSTITCVSGFSLTSGYGVHVRQSPGKGLEWLVG 69
DB 10 LVALLRGVOCVOLVSEGGVQVPGHRSLSLCAASGFTFSSYGHHVWRQAPGKLEWVAV 69
QY 70 IWSGGDTYNAAFI-SRLSTISKDNRKSQLFFKKNLSRATDTAIYYCAR-----NRGDI 121
DB 70 ISNDGDNKYHADSVWGRFTISRDNRSRTLYLQNNLSRAEDTAIYYCARRGMGSGSGRGDY 129
QY 122 YDFTYAMDYWGQGTSTVTVSSAKTTTPSYVPLAPGCGDTTSSVTLGLCVKGYFPESVTV 181
DB 130 YY--YVGLDWGQGTTVTVSSASTKGPSVFLPACRSRSTSESTAALGCLVKDYFPEPTV 187
QY 182 TWNSGSLSSVHTFPALLO-SGLYTMSSSVTVPSSTWSPQTVTCVAHPASSTVVDKLE 240
DB 188 SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYTCNVDRHPSNTKVKDQTV 247
QY 241 PSGPSTINPCPCKECHKCAPNLEGGSVTFPPNIDVLMISUTPKVTCVVVDVSD 300
DB 248 -----RKC--CVCEPCPPAPPV-AGPSVFLFPKPKDRLMISRTPEVTCVVVDVSH 296
QY 301 DPDVOLSWFNVNVEHTAQTOTHREDYNSTIRVWSTPLTQHODWMSGKFKCVNNKDL 360
DB 297 DPEVGFNIVDGVGVHNAKTPREQFNSTFRVSVLTVVHODWLNKGYCKKCVSNKGLP 356
QY 361 SPIERTISKIGLVRAPQVYILPPPAEQLSRKDVSLTCLWGFNPGDISVWNTSGHTE 420
DB 357 APIETISKTKGQPREQVYTLPPSREEMTKNOVSLTCLVKGYFSPDIAVWESNGQ 416
QY 421 NYKOTAPVLDSGTYFYISKLNMTSKNEKTDTSFCNVRHEGLKNYLLKTTISRSPGK 478
DB 417 NYKTPPMLDSGDFLYSKLTVDKSRWQCGNVFSCVMHEALHNHYTQKLSLSLSPGK 474

RESULT 14
US-10-272-899A-80
; Sequence 80, Application US/10272899A
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBIOTIC CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MPI01-244P2M
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin cassette protein sequence
; OTHER INFORMATION: Leader-Mu_FCR11_61
; US-10-272-899A-80

Query Match 56.9%; Score 1452.5; DB 6; Length 361;
Best Local Similarity 59.4%; Pred. No. 5e-86;

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179 VSWNGALTSVHTFPAVLQSSGLSYLSSVTVVPSSNEGTQTYTCNVNDHKPSNTKVDKTV 238  
240 EPSGPISTINPCPCKECHKCPAPNLEGGPSVFIPPPNKKDVLMIKSLTPKVTVCVVVDYSE 299  
239 E-----RKC--CVECPCPAPV-AGPSVFLPPPKDLMISRTPEVTCVVVDYSH 287  
300 DDPDVQISMFVNNVEVHTAQOTQTHREDYNSTIRVVSTLPIQHODMMSGKEFKCKVNNKDL 359  
288 EDPEVQFNWYVDGVEVHNAKTPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGL 347  
360 PSPIERTISKGLVRAPQVYILPPPAQLSRKDYSLTCLVVGFPNPGDISVWTSNGHTE 419  
348 PAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 407  
420 ENYKDTAPVLDSGYSFYISKLNMKTSKWEKTDSCNVRHEGLKNYLLKKTISRSPGK 478  
408 NNYKTPPMLDSGFFLYSLTVDKSRWQGNVTFSCVMHEALHNHYTKSLSLSPGK 466

Search completed: June 18, 2003, 16:48:36  
Job time : 59.3933 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 18, 2003, 16:44:27 ; Search time 296.065 Seconds  
(without alignments)  
1040.930 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLFLCLTFPSCVLSQ.....RHEGLKNLYLKKTISRSPGK 478

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

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12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pcp.\*

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27: /cgn2\_6/ptodata/1/paa/US103\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	2552	100.0	478	21	US-09-770-916-2
2	2083.5	81.6	454	20	US-09-770-916-2
3	2083.5	81.6	462	20	US-09-770-916-2
4	2082	81.6	457	21	US-09-770-916-2
5	2067	81.0	474	21	US-09-770-916-2
6	2024.5	79.3	475	21	US-09-770-916-2

7	1802	70.6	336	21	US-09-770-916-2	Sequence 26476, A
8	1798	70.5	335	21	US-09-770-916-2	Sequence 40387, A
9	1797	70.4	405	21	US-09-770-916-2	Sequence 26475, A
10	1793	70.3	404	21	US-09-770-916-2	Sequence 40389, A
11	1784	69.9	336	21	US-09-770-916-2	Sequence 62004, A
12	1778	69.7	336	21	US-09-770-916-2	Sequence 40377, A
13	1751	68.6	468	3	US-07-743-329-7	Sequence 7, Appli
14	1751	68.6	468	7	US-08-303-569-7	Sequence 7, Appli
15	1751	68.6	468	8	US-08-485-686-7	Sequence 7, Appli
16	1751	68.6	468	17	US-09-348-224-7	Sequence 7, Appli
17	1742	68.3	468	12	US-08-846-658A-7	Sequence 7, Appli
18	1742	68.3	468	12	US-08-846-658B-7	Sequence 7, Appli
19	1742	68.3	468	21	US-09-795-515-7	Sequence 7, Appli
20	1739	68.1	446	21	US-09-791-537-12231	Sequence 12331, A
21	1727.5	67.7	469	8	US-08-462-767-2	Sequence 2, Appli
22	1727.5	67.7	469	21	US-09-791-537-126760	Sequence 126760, A
23	1725.5	67.6	444	21	US-09-791-537-87449	Sequence 87449, A
24	1725.5	67.6	461	21	US-09-791-537-28655	Sequence 28655, A
25	1648	64.6	437	21	US-09-791-537-52926	Sequence 52926, A
26	1643	64.4	468	24	US-10-058-120-12	Sequence 12, Appli
27	1596	62.5	476	19	US-09-584-166B-12	Sequence 12, Appli
28	1580.5	61.9	446	20	US-09-618-380-7	Sequence 7, Appli
29	1547.5	60.6	457	21	US-09-791-537-112963	Sequence 112963, A
30	1528	59.9	470	21	US-09-791-537-56006	Sequence 56006, A
31	1519.5	59.5	472	21	US-09-791-537-29038	Sequence 29038, A
32	1497.5	58.7	464	1	PCT-USQ1-14151-23	Sequence 23, Appli
33	1486	58.2	461	7	US-08-338-503-2	Sequence 2, Appli
34	1486	58.2	444	21	US-09-791-537-34061	Sequence 34061, A
35	1485.5	58.2	444	21	US-09-791-537-152190	Sequence 152190, A
36	1484	58.2	599	6	US-08-267-641-18	Sequence 18, Appli
37	1484	58.2	599	13	US-08-949-382-18	Sequence 18, Appli
38	1482	58.1	460	8	US-08-480-120-2	Sequence 2, Appli
39	1472	57.7	456	20	US-09-613-017-2	Sequence 2, Appli
40	1472	57.7	456	23	US-09-903-327A-2	Sequence 2, Appli
41	1472	57.7	464	14	US-09-053-583-9	Sequence 9, Appli
42	1472	57.7	464	18	US-09-408-646-9	Sequence 9, Appli
43	1472	57.7	464	18	US-09-499-662-9	Sequence 9, Appli
44	1472	57.7	464	26	US-10-216-484-9	Sequence 9, Appli
45	1471.5	57.7	458	21	US-09-791-537-89130	Sequence 89130, A

## ALIGNMENTS

## RESULT 1

US-09-770-916-2  
; Sequence 2, Application US/09770916  
; GENERAL INFORMATION:

; APPLICANT: Frank, Dara W.

; APPLICANT: Wiener-Kronish, Jeannine

; APPLICANT: Yahr, Timothy L.

; APPLICANT: Sawa, Teiji

; APPLICANT: Fritz, Robert B.

; TITLE OF INVENTION: Method of and compositions for immunization with the

; FILE REFERENCE: 650053.91487

; CURRENT APPLICATION NUMBER: US/09770,916

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/448,339

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 60/109,952

; PRIOR FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/126,794

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 478

; TYPE: PRT

; ORGANISM: mouse

US-09-770-916-2

Query Match 100.0%; Score 2552; DB 21; Length 478;

Best Local Similarity 100.0%; Pred. No. 7.8e-200; Indels 0; Gaps 0;  
Matches 478; Conservative 0; Mismatches 0;

1 MAVLGLLFCLVTFPSCVLSQVQLKQSGFLVQPSQSLITCTVSGFSLTSYGVHVRQSP 60  
1 MAVLGLLFCLVTFPSCVLSQVQLKQSGFLVQPSQSLITCTVSGFSLTSYGVHVRQSP 60  
61 GKLEWLGVIWGGDGTNYAFAISRLSISKDNKSQLEFFKMNLSRATDTAIYYCARNRGD 120  
61 GKLEWLGVIWGGDGTNYAFAISRLSISKDNKSQLEFFKMNLSRATDTAIYYCARNRGD 120  
121 IYDFTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPCGDGTGSSVTGLCLVKGYFPESVT 180  
121 IYDFTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPCGDGTGSSVTGLCLVKGYFPESVT 180  
181 VTWNSGSLSSSVHTFPALLOGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKKLE 240  
181 VTWNSGSLSSSVHTFPALLOGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKKLE 240  
241 PSGPTISTINPCPPCKECHKCAPNLEGGPSVFIFPPNPKDVLIMISLTPKVTCTVVAHPASSTTVDDKKLE 300  
241 PSGPTISTINPCPPCKECHKCAPNLEGGPSVFIFPPNPKDVLIMISLTPKVTCTVVAHPASSTTVDDKKLE 300  
301 DPVQISWFWNNVEVHTAQTQTHREDYNTIRVSTLPIQHODMWSGKEFKCKVNNKDL 360  
301 DPVQISWFWNNVEVHTAQTQTHREDYNTIRVSTLPIQHODMWSGKEFKCKVNNKDL 360  
361 SPIERTISKIKGLVRAPQVYILPPAEQLSRKDVSLTCLVGVFNPGDISVETNSNGHTEE 420  
361 SPIERTISKIKGLVRAPQVYILPPAEQLSRKDVSLTCLVGVFNPGDISVETNSNGHTEE 420  
421 NYKDPAPVLDSDGSGYFIYKLNKMTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 478  
421 NYKDPAPVLDSDGSGYFIYKLNKMTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 478

RESULT 2  
Sequence 4, Application US/09653755A  
GENERAL INFORMATION:  
APPLICANT: Eisinger, Dominic P.  
APPLICANT: Stiles, Lynn  
APPLICANT: Lamarche, Arthur  
APPLICANT: Jelinek, Thomas  
TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for  
TITLE OF INVENTION: Phosphotyrosine-Containing Proteins  
FILE REFERENCE: 724650-3  
CURRENT APPLICATION NUMBER: US/09/653,755A  
CURRENT FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
OTHER INFORMATION: sequence for heavy chain of recombinant antibody  
US-09-653-755A-4

Query Match 81.6%; Score 2083.5; DB 20; Length 454;  
Best Local Similarity 84.8%; Pred. No. 1.8e-161;  
Matches 391; Conservative 26; Mismatches 35; Indels 9; Gaps 3;

20 QVQLKQSGFLVQPSQSLITCTVSGFSLTSYGVHVRQSPKGLWLGVI--WSGGDT 77  
1 EVQLQSGPELVKPGASVMISRTSAYTFTENTVHWVKQSHGESLEWIGGINPYGGSI- 59  
78 YNAAFISRLSISKDNKSQLEFFKMNLSRATDTAIYYCARNRGDIYDYFTYAMDYWGQGT 137  
60 FSPKFKGKATLVTDKSSSTAYMELSLTSEDSAVYYCARRAGAYF-----DYWGQGT 113  
138 VTVSSAKTTPPSVYPLAPCGDGTGSSVTGLCLVKGYFPESVTVTWNSGSLSSSVHTFPA 197

114 LTVSSAKTTPPSVYPLAPCGDGTGSSVTGLCLVKGYFPESVTVTWNSGSLSSSVHTFPA 173  
198 LQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 257  
174 LQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 233  
258 HKCAPNLEGGPSVFIFPPNPKDVLIMISLTPKVTCTVVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 317  
234 HKCAPNLEGGPSVFIFPPNPKDVLIMISLTPKVTCTVVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 293  
318 AQTQTHREDYNTIRVSTLPIQHODMWSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377  
294 AQTQTHREDYNTIRVSTLPIQHODMWSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 353  
378 QVYILPPAEQLSRKDVSLTCLVGVFNPGDISVETNSNGHTEEYKDTAPVLDSDGSGYFI 437  
354 QVYILPPAEQLSRKDVSLTCLVGVFNPGDISVETNSNGHTEEYKDTAPVLDSDGSGYFI 413  
438 YSKLNKMTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 478  
414 YSKLNKMTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 454

RESULT 3  
US-09-653-755A-6  
Sequence 6, Application US/09653755A  
GENERAL INFORMATION:  
APPLICANT: Eisinger, Dominic P.  
APPLICANT: Stiles, Lynn  
APPLICANT: Lamarche, Arthur  
APPLICANT: Jelinek, Thomas  
TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for  
TITLE OF INVENTION: Phosphotyrosine-Containing Proteins  
FILE REFERENCE: 724650-3  
CURRENT APPLICATION NUMBER: US/09/653,755A  
CURRENT FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 462  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
OTHER INFORMATION: sequence for heavy chain of recombinant antibody  
OTHER INFORMATION: with C-terminal histidine tag sequence  
US-09-653-755A-6

Query Match 81.6%; Score 2083.5; DB 20; Length 462;  
Best Local Similarity 84.8%; Pred. No. 1.8e-161;  
Matches 391; Conservative 26; Mismatches 35; Indels 9; Gaps 3;

20 QVQLKQSGFLVQPSQSLITCTVSGFSLTSYGVHVRQSPKGLWLGVI--WSGGDT 77  
1 EVQLQSGPELVKPGASVMISRTSAYTFTENTVHWVKQSHGESLEWIGGINPYGGSI- 59  
78 YNAAFISRLSISKDNKSQLEFFKMNLSRATDTAIYYCARNRGDIYDYFTYAMDYWGQGT 137  
60 FSPKFKGKATLVTDKSSSTAYMELSLTSEDSAVYYCARRAGAYF-----DYWGQGT 113  
138 VTVSSAKTTPPSVYPLAPCGDGTGSSVTGLCLVKGYFPESVTVTWNSGSLSSSVHTFPA 197  
114 LTVSSAKTTPPSVYPLAPCGDGTGSSVTGLCLVKGYFPESVTVTWNSGSLSSSVHTFPA 173  
198 LQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 257  
174 LQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 233  
258 HKCAPNLEGGPSVFIFPPNPKDVLIMISLTPKVTCTVVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 317  
234 HKCAPNLEGGPSVFIFPPNPKDVLIMISLTPKVTCTVVAHPASSTTVDDKKLEPSGPISTINPCPPCKEC 293

QY 318 AOTQTHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIGLVRA 377  
Db 294 AOTQTHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIGLVRA 353  
QY 378 QYVILPPPAEQLSRKDVSLTCLVGFNPGDISVWETSNHTEENYKDTAPVLDSDGSYFI 437  
Db 354 QYVILPPPAEQLSRKDVSLTCLVGFNPGDISVWETSNHTEENYKDTAPVLDSDGSYFI 413  
QY 438 YSKLNMTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 478  
Db 414 YSKLNMTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 454

RESULT 4  
US-09-791-537-127944  
; Sequence 127944, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 127944  
; LENGTH: 457  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-127944

Query Match 81.6%; Score 2082; DB 21; Length 457;  
Best Local Similarity 84.3%; Pred. No. 2.4e-161;  
Matches 388; Conservative 31; Mismatches 37; Indels 4; Gaps 2;  
QY 20 QVQLKQSGPGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKGLWLGVIWVSGGD-TDY 78  
Db 1 EVQLQSGAEVLRGTSVKMCKKAAGYFTFTNYIGWIKEREGHLEWIGDIYPGGGFTNY 60  
QY 79 NAAFIISRLSISKNSKSLQFFKXKNSLRATDAIYYCARNRGGDIYDYFTYAMDYWGQTSV 138  
Db 61 NENFKGKATLTADTSSTAYAYQLSSLSSEDAIYHCARG---IYNSSPYFDSWGQGTLL 117  
QY 139 TVSSAKTTPPSVYPLAPCGGDTTGSSTVGLGVKGYFPESVTVTNWNSGSLSSSVHTFPAL 198  
Db 118 TVSSAKTTPPSVYPLAPCGGDTTGSSTVGLGVKGYFPESVTVTNWNSGSLSSSVHTFPAL 177  
QY 199 LQSGLYTMSSSVTPSPSTWPSQTVCVAHPASSTTVDDKLEPSGPISTINPCPPCKECH 258  
Db 178 LQSGLYTMSSSVTPSPSTWPSQTVCVAHPASSTTVDDKLEPSGPISTINPCPPCKECH 237  
QY 259 KCPAPNLEGGSPVFIAPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWVFNVEVHTA 318  
Db 238 KCPAPNLEGGSPVFIAPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWVFNVEVHTA 297  
QY 319 QTOHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPO 378  
Db 298 QTOHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPO 357  
QY 379 VYILPPPAEQLSRKDVSLTCLVGFNPGDISVWETSNHTEENYKDTAPVLDSDGSYFI 438  
Db 358 VYILPPPAEQLSRKDVSLTCLVGFNPGDISVWETSNHTEENYKDTAPVLDSDGSYFI 417  
QY 439 SKLNMTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 478  
Db 418 SKLNMTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 457

RESULT 5  
US-09-791-537-54066  
; Sequence 54066, Application US/09791537

; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 54066  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-54066

Query Match 81.0%; Score 2067; DB 21; Length 474;  
Best Local Similarity 83.8%; Pred. No. 4.3e-160;  
Matches 389; Conservative 29; Mismatches 38; Indels 8; Gaps 4;  
QY 17 VLQVQLKQSGPGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKGLWLGVIWVSGGD- 75  
Db 17 VHSEVQLQSGPGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKGLWLGVIWVSGGD- 76  
QY 76 TDYNAAFISRLSISKNSKSLQFFKXKNSLRATDAIYYCARNRGGDIYDYFTYAMDYWGQ 135  
Db 77 TKFNEKFKGKATLTSDKSSNTAYMELSSLSLTSVSAVYYCARD-----YDYDW-FAYWGQ 130  
QY 136 TSVTVSSAKTTPPSVYPLAPCGGDTTGSSTVGLGVKGYFPESVTVTNWNSGSLSSSVHTF 195  
Db 131 TLVTVSSAKTTPPSVYPLAPCGGDTTGSSTVGLGVKGYFPESVTVTNWNSGSLSSSVHTL 190  
QY 196 -PALQSGLYTMSSSVTPSPSTWPSQTVCVAHPASSTTVDDKLEPSGPISTINPCPPC 254  
Db 191 SQALLQSGLYTMSSSVTPSPSTWPSQTVCVAHPASSTTVDDKLEPSGPISTINPCPPC 250  
QY 255 KECHKCAPNLEGGSPVFIAPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWVFNVE 314  
Db 251 KECHKCAPNLEGGSPVFIAPPNIKDVLMISLTPKVTVCVVDVSEDDPDVQISWVFNVE 310  
QY 315 VHTAQTHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIGLV 374  
Db 311 VHTAQTHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIGLV 370  
QY 375 RAPQYVILPPPAEQLSRKDVSLTCLVGFNPGDISVWETSNHTEENYKDTAPVLDSDGS 434  
Db 371 RAPQYVILPPPAEQLSRKDVSLTCLVGFNPGDISVWETSNHTEENYKDTAPVLDSDGS 430  
QY 435 YFIYSKLNMTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 478  
Db 431 YFIYSKLNMTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 474

RESULT 6  
US-09-791-537-126419  
; Sequence 126419, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 126419  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-126419



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; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26475
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-26475

Query Match
Best Local Similarity 100.0%; Score 1797; DB 21; Length 405;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

143 AKTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 202
1 AKTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 240
383 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
241 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 477
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 335

RESULT 10
US-09-791-537-40389
Sequence 40389, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 40389
LENGTH: 404
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-40389

Query Match
Best Local Similarity 100.0%; Score 1793; DB 21; Length 404;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

144 KTTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 203
1 KTTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
204 YTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPAP 263
61 YTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPAP 120
264 NLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 323
1 NLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 240
383 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
241 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336

RESULT 12
US-09-791-537-40377
Sequence 40377, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62004
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-62004

Query Match
Best Local Similarity 69.9%; Score 1784; DB 21; Length 336;
Matches 332; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

143 AKTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 202
1 AKTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 240
383 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
241 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336

RESULT 11
US-09-791-537-62004
Sequence 62004, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62004
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-62004

Query Match
Best Local Similarity 98.8%; Score 1784; DB 21; Length 336;
Matches 332; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

143 AKTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 202
1 AKTTPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFPPNPKDVLMSLTPTKVCVVVDVSEDDPDVQISWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 240
383 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
241 PPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336
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FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791,537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 40377  
LENGTH: 336  
TYPE: PRT  
ORGANISM: Mus musculus  
-09-791-537-40377

Query Match 69.7%; Score 1778; DB 21; Length 336;  
Best Local Similarity 98.8%; Pred. No. 1.3e-136;  
Matches 332; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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|||||  
1 AKTTPPSVYIPLAPCGDGTGSSVTLGCLVKGYPFVSIVTWNSSLSSTVTFPALLQSG 60  
|||||  
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLEPSPGPISTINPCPCKECHKCPA 262  
|||||  
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLEPSPGPISTINPCPCKECHKCPA 120  
|||||  
263 PNLEGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDVQISWFVNNVEVHTAQQT 322  
|||||  
121 PNLEGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDVQISWFVNNVEVHTAQQT 180  
|||||  
323 HREDYNSTIRVSTLPIQHQDMGSKGKCKVNNKDLPSPIERTISKGLVRAPOVYIL 382  
|||||  
181 HREDYNSTIRVSHLPIQHQDMGSKGKCKVNNKDLPSPIERTISKGLVRAPOVYIL 240  
|||||  
383 PPPAQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442  
|||||  
241 PPPAQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300  
|||||  
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPGK 478  
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301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPGK 336  
|||||

## RESULT 13

-09-743-329-7

Sequence 7, Application US/07743329

## GENERAL INFORMATION:

APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Entage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/743,329  
FILING DATE: 19910917

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: CARP-0009  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-743-329-7

Query Match 68.6%; Score 1751; DB 3; Length 468;  
Best Local Similarity 69.0%; Pred. No. 3.3e-134;  
Matches 327; Conservative 60; Mismatches 75; Indels 12; Gaps 4;

QY 6 LLFCLVTFPSCVQLSQVQLQSGPLVQPSQSILITCTVSGFSLTSYGVHVHQSPGKLE 65  
|||  
DB 6 IFLLLSVTAGVHSGVQLQSGAELARPGASVKMSKASGYTFTRYTHMWVKRQPGQGLE 65  
|||  
QY 66 WLGI-VSGGDTDYNAAFISRLSISKDNKSKSOLFPMKNSLRATDTAIYYCARNRDIYD 124  
|||  
DB 66 WIGYINPSRGYTNQKFKDKATLTDDKSSSTAYMQLSLSLTSEDNAVYYCAR-----YD 120  
|||  
QY 125 FTYAMDYWGQGTSTVTVSSAKTTPPSVYIPLAPCGDGTGSSVTLGCLVKGYPFVSIVTWN 184  
|||  
DB 121 DHYCLDYWGQGTSTVTVSSAKTTPPSVYIPLAPCGDGTGSSVTLGCLVKGYPFVSIVTWN 180  
|||  
QY 185 SGLSSSVHTFPALLOSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLEPSPG 244  
|||  
DB 181 SGLSSSVHTFPALLOSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLEPSPG 240  
|||  
QY 245 1STINPCPCKECHKCPAPNLEGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDV 304  
|||  
DB 241 --TKPCPC---KCPAPNLLGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDV 294  
|||  
QY 305 QISWFVNNVEVHTAQTHREDYNSTIRVSTLPIQHQDMGSKGKCKVNNKDLPSPIE 364  
|||  
DB 295 QISWFVNNVEVHTAQTHREDYNSTIRVSTLPIQHQDMGSKGKCKVNNKDLPSPIE 354  
|||  
QY 365 RTISKIGLVRAPOVYILPPPAQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYK 424  
|||  
DB 355 RTISKPGSVRAPOVYILPPPEEEMTKQVTLTCMTDFMVDIYVETNNGKTELNYKN 414  
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QY 425 TAPVLDSDGSYFIYSKLNKMTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPGK 478  
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DB 415 TEPVLDSDGSYFIYSKLNKMTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPGK 468  
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## RESULT 14

US-08-303-569-7

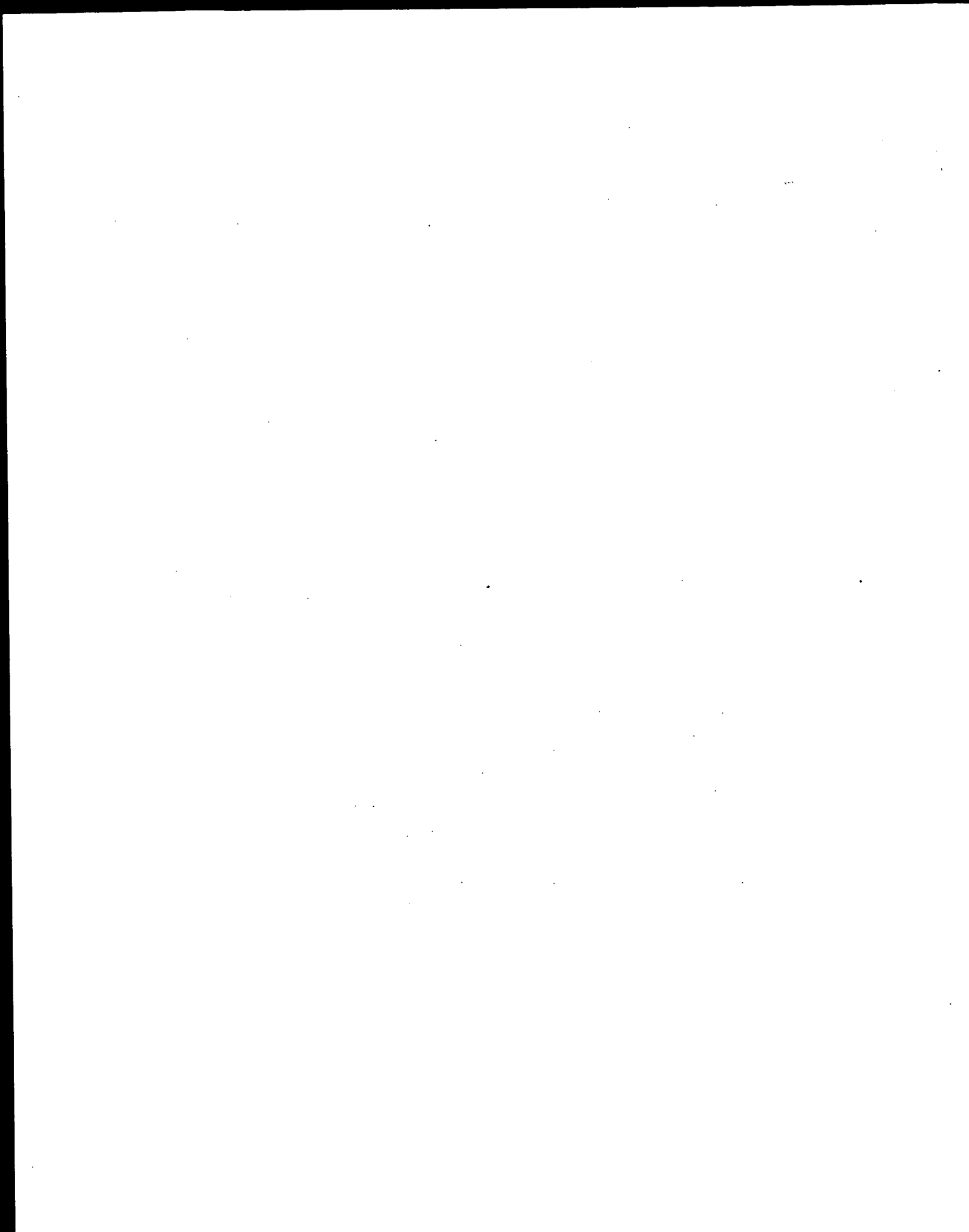
Sequence 7, Application US/08303569

## GENERAL INFORMATION:

APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Entage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303,569  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/743,329  
FILING DATE: 17-SEP-1991  
ATTORNEY/AGENT INFORMATION:







GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 18, 2003, 16:46:17 ; Search time 44.9803 Seconds  
(without alignments)  
1149.899 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLFLVFFSCVLSQ.....RHEGLKNTYKTKTSRPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published\_Applications\_AA:\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1742	68.3	468	9	US-09-795-515-7
2	1472	57.7	456	9	US-09-903-327A-2
3	1472	57.7	464	9	US-10-216-484-9
4	1458	57.1	451	9	US-10-153-382-17
5	1456.5	57.1	452	9	US-09-726-258-71
6	1452.5	56.9	551	10	US-09-815-837-93
7	1445	56.6	476	9	US-10-124-905-12
8	1445	56.6	476	9	US-09-948-429B-12
9	1440	56.4	451	10	US-09-822-698A-26
10	1439.5	56.4	475	10	US-09-740-002-27
11	1434	56.2	470	9	US-10-020-786-9
12	1434	56.2	470	9	US-10-227-694-5
13	1432	56.1	464	9	US-10-153-382-9
14	1430.5	56.1	450	9	US-09-996-288-220
15	1430.5	56.1	450	9	US-09-996-265-220
16	1430.5	56.1	450	10	US-09-796-848A-37
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18	1430.5	56.1	463	9	US-10-153-382-13
19	1430.5	56.1	475	10	US-09-740-002-25

20 1429.5 56.0 467 9 US-10-211-357-12  
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22 1424.5 55.8 444 9 US-10-150-475A-6  
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27 1424.5 55.8 450 10 US-09-796-848A-39  
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43 1422.5 55.7 450 9 US-09-996-288-244  
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45 1422.5 55.7 450 9 US-09-996-265-210

## ALIGNMENTS

## RESULT 1

US-09-795-515-7  
; Sequence 7, Application US/09795515  
; Publication No. US20030039645A1  
; GENERAL INFORMATION:  
; APPLICANT: Adair, John R.  
; APPLICANT: Athwal, Diljeet S.  
; APPLICANT: Entage, John S.  
; TITLE OF INVENTION: Humanised Antibodies  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/795,515  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,658  
; FILING DATE: 01-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trujillo, Doreen Yathko  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0057  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein





316 HTAQTHREDYNSTIRVVSTLP IQH QDWM SGEF ECKV NKNK DLP SIERTIS IKGLVR 375

QY 119 -----GDIYDFTIANDYWGQGTSTVTVSSAKTTPSPVPLAPGCGDTTGGSSVTLGCLVKG 171

Db 121 LFSVGVGNVNNW---FDVWPGVGLVTVSSASTKGPVFLAPSSKSTSGTAALGCLVKD 177  
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Db 178 YPEPVTWNSGALTSVHTFPALQSSGLYSLSSVTPVSSSLGTQYICNVNHPKN 237  
QY 233 TVVDKLEPSGPISTINCPCKECHKCPAPNLEGSPVFIIPPNIKDVLMISLTPKVTC 292  
Db 238 TKVDKKAEPKCDKT-HTCPCP-----CPAPELLGGPSVFLPPPKDPLMISRTPEVTC 290  
QY 293 VVDVSEDDPDVQISWFWNNVHTAQTOTHRDYNSTIRVYSTLPQIHOHDMGSKFKC 352  
Db 291 VVDVSHEDPEVKFNWYDGVVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKC 350  
QY 353 KYNKDLPSPIERTISKIGLVRAPQVYILPPAPQLSKDKVSLTCLVVGPNPGDISVEM 412  
Db 351 KYSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 410  
QY 413 TSNHGTEENYKDTAPVLDSGSGSYFIYSKLNMTSKWEKTDSCNVRHGKLNYYLKRTI 472  
Db 411 ESNQGPENNYKTPPVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSL 470  
QY 473 SRSPCK 478  
Db 471 SLSPCK 476

## RESULT 8

US-09-948-429B-12  
; Sequence 12, Application US/09948429B  
; Patent No. US20020177689A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/948,429B  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021

## INFORMATION FOR SEQ ID NO:

12:

## SEQUENCE CHARACTERISTICS:

LENGTH: 476 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

S-09-948-429B-12

Query Match 56.6%; Score 1445; DB 9; Length 476;

Best Local Similarity 57.8%; Pred. No. 2.5e-73;

Matches 281; Conservative 72; Mismatches 115; Indels 18; Gaps 7;

QY 1 MAVLGHLFCLVTPFSCVLSQVQLKQSGPGLVQPSSLSITCTVSGFSLT-SYGVHWVRQS 59

Db 1 MKHLWFEFLLLVAAPRWLVLSQVQLQESGPGLVKPELSEILSLTCAVSGGSGISGCGYWGWIROP 60

QY 60 PGKGLWGLVIW-SGGDTYNAAFISRLSISKDNKSQQLFFKMNLSRADTATYYICARNR 118

Db 61 PGKGLWIGISFYSSSGNTYYNPSLKSQVITSTDTSKNQFSLKLSNMTAADAATVAVYCVDR 120

QY 119 ----GDIYDFTYMDYWGCGTSVTVSSAKITPPSVYVLPAGCGDTTGTSSVTLGCLVK 173

Db 121 LFSVGVGNVNNW---FDVWPGVGLVTVSSASTKGPVFLAPSSKSTSGTAALGCLVKD 177

QY 174 YPESVTVWNSGSLSSSVHTFPALQ-SGLYTMSSSVTPSPSTWPSQTWTCVSAHPASS 232

Db 178 YPEPVTWNSGALTSVHTFPALQSSGLYSLSSVTPVSSSLGTQYICNVNHPKN 237

QY 233 TVVDKLEPSGPISTINCPCKECHKCPAPNLEGSPVFIIPPNIKDVLMISLTPKVTC 292

Db 238 TKVDKKAEPKCDKT-HTCPCP-----CPAPELLGGPSVFLPPPKDPLMISRTPEVTC 290

QY 293 VVDVSEDDPDVQISWFWNNVHTAQTOTHRDYNSTIRVYSTLPQIHOHDMGSKFKC 352

Db 291 VVDVSHEDPEVKFNWYDGVVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKC 350

QY 353 KYNKDLPSPIERTISKIGLVRAPQVYILPPAPQLSKDKVSLTCLVVGPNPGDISVEM 412

Db 351 KYSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 410

QY 413 TSNHGTEENYKDTAPVLDSGSGSYFIYSKLNMTSKWEKTDSCNVRHGKLNYYLKRTI 472

Db 411 ESNQGPENNYKTPPVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSL 470

QY 473 SRSPCK 478

Db 471 SLSPCK 476

## RESULT 9

US-09-822-698A-26  
; Sequence 26, Application US/09822698A  
; Patent No. US20020146750A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 26  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-IgG1  
US-09-822-698A-26

Query Match 56.4%; Score 1440; DB 10; Length 451;

Best Local Similarity 59.9%; Pred. No. 4.5e-73;

Matches 276; Conservative 67; Mismatches 106; Indels 12; Gaps 5;

QY 20 QVQLKQSGPGLVQPSSLSITCTVSGFSLTSYGVHWVRQSPGKGLWLG-VVIWSGGDTDY 78

Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSGTYY 60









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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:42:37 ; Search time 23.4972 Seconds  
(without alignments)  
598.546 Million cell updates/sec

Title: US-09-770-916-2  
Perfect score: 2552  
Sequence: 1 MAVLGLLCLVTFPSCVLSQ.....RHEGLKNYKLTISRPOK 478

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1751	68.6	468	2	US-08-116-247-7
2	1742	68.3	468	2	US-08-303-569B-7
3	1580.5	61.9	446	3	US-08-397-411-7
4	1515	59.4	464	1	US-08-353-400-36
5	1506	59.0	445	1	US-08-353-400-33
6	1484	58.2	599	1	US-08-442-542-18
7	1484	58.2	599	3	US-08-765-469-18
8	1471.5	57.7	473	4	US-09-049-672A-4
9	1460	57.2	447	6	5455030-1
10	1456.5	57.1	452	3	US-09-027-449-71
11	1456.5	57.1	452	4	US-09-026-985-71
12	1456.5	57.1	452	4	US-09-121-952A-71
13	1456.5	57.1	452	4	US-09-234-340A-71
14	1445	56.6	476	3	US-08-487-550-12
15	1429.5	56.0	467	4	US-08-523-894-10
16	1428	56.0	467	4	US-08-793-450-8
17	1422.5	55.7	449	4	US-09-679-397-2
18	1422.5	55.7	449	4	US-09-680-148-2
19	1422.5	55.7	467	4	US-08-523-894-10
20	1422	55.7	451	2	US-08-887-352B-14
21	1422	55.7	451	2	US-08-887-352B-16
22	1422	55.7	451	2	US-08-887-352B-18
23	1422	55.7	451	3	US-08-466-151-65
24	1422	55.7	451	4	US-09-109-207C-14
25	1422	55.7	451	4	US-09-109-207C-16
26	1422	55.7	451	4	US-09-109-207C-18
27	1422	55.7	451	4	US-09-282-505-2

28	1422	55.7	451	4	US-09-054-255-2	Sequence 2, Appli
29	1422	55.7	451	4	US-09-296-005-14	Sequence 14, Appl
30	1422	55.7	451	4	US-09-296-005-16	Sequence 16, Appl
31	1422	55.7	451	4	US-09-296-005-18	Sequence 18, Appl
32	1416	55.5	476	3	US-08-487-550-4	Sequence 4, Appli
33	1414.5	55.4	467	4	US-08-523-894-8	Sequence 8, Appli
34	1405	55.1	443	5	PCT-US96-13152-4	Sequence 4, Appli
35	1404.5	55.0	467	1	US-08-704-744-81	Sequence 81, Appl
36	1403	55.0	467	4	US-09-049-672A-8	Sequence 8, Appli
37	1401	54.9	472	4	US-09-301-593-30	Sequence 30, Appl
38	1400.5	54.9	453	4	US-09-301-593-18	Sequence 18, Appl
39	1400.5	54.9	469	2	US-07-934-373C-23	Sequence 23, Appl
40	1400.5	54.9	469	3	US-08-437-642B-23	Sequence 23, Appl
41	1400.5	54.9	469	4	US-08-146-206C-23	Sequence 23, Appl
42	1400	54.9	453	3	US-08-466-151-8	Sequence 8, Appli
43	1400	54.9	453	4	US-08-466-163B-8	Sequence 8, Appli
44	1399.5	54.8	459	1	US-08-157-101A-7	Sequence 7, Appli
45	1399.5	54.8	552	5	PCT-US93-07832-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-08-116-247-7  
; Sequence 7, Application US/08116247  
; Patent No. 5929212  
; GENERAL INFORMATION:  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Zivin, Robert A.  
; APPLICANT: Adair, John R.  
; APPLICANT: Athwal, Diljeet S.  
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,247  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/743,377  
; FILING DATE: 10-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paintin, Francis A.  
; REGISTRATION NUMBER: 19,386  
; REFERENCE/DOCKET NUMBER: CARP-0011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-116-247-7

Query Match 68.6%; Score 1751; DB 2; Length 468;  
Best Local Similarity 69.0%; Pred. No. 3.6e-132;  
Matches 327; Conservative 60; Mismatches 75; Indels 12; Gaps 4;  
QY 6 LLFCLVFPSCVLSQVQLKQSGPGLVDPQSLSITCTVSGFSLTSYGVHWRQSPGKGL 65

6 IFLLLSVTAGVHSGVQLQSGAELARPGASVKMSCKASGYTFYTRTMHWVKRPGQGLE 65  
66 WLGI-V-WSGGDTDNAAFISSLISKONSKSOLPFKMSLRATDTAIYVCARNRGGDIYD 124  
66 WIGYNPSRGVNTNPKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVIYCAR-----YYD 120  
125 FTYAMDYWGQGTSTVTSVSAKTTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPPESVTVTN 184  
121 DRYCLDYWGQGTSTVTSVSAKTTAPSVYPLAPVCGDGTGSSVTLGCLVKGYPPVPTLTWN 180  
185 SGSLSSSVHTFPALQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKLEPSPG 244  
181 SGSLSSSVHTFPALQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKLEPSPG 240  
245 ISTINPCPCKECHKCAPNLEGSPSVFIFPPNIDKVLMSITLTPKVTGVVDVSDDDPDV 304  
241 --TIKPCPC-----KCAPNLLGGSPVFIFPPNIDKVLMSITLTPKVTGVVDVSDDDPDV 294  
305 QISWFWNNVEVHTAQTQTHREDYNSITIRVWSTLPIQHDQMSGKEFKCKVNNKDLPSPIE 364  
295 QISWFWNNVEVHTAQTQTHREDYNSITIRVWSTLPIQHDQMSGKEFKCKVNNKDLPSPIE 354  
365 RTISKIKGLVRAPQVYVILPPPAEQLSRKDVSLTCLVGVGNPGDISVWTSNGHTEENYKD 424  
355 RTISKPKGSVRAPQVYVILPPPEEEMTKQVLTLCVMTDFMPEDIIYVETNNGKTELNYKN 414  
425 TAPVLDSGSGFYIYKLNKMTSKWEKTSFSCNVRHGLKNYLYLKKTISRSPGK 478  
415 TEPVLDSGSGFYIYKLNKMTSKWEKTSFSCNVRHGLKNYLYLKKTISRSPGK 468

RESULT 2

3-08-303-569B-7  
Sequence 7, Application US/08303569B  
Patent No. 5859205  
GENERAL INFORMATION:  
APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Emtage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303,569B  
FILING DATE: 07-SEP-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Trujillo, Doreen Yanko  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CARP-0032  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-08-303-569B-7

Query Match 68.3%; Score 1742; DB 2; Length 468;  
Best Local Similarity 68.8%, Pred. No. 1.9e-131;  
Matches 326; Conservative 60; Mismatches 76; Indels 12; Gaps 4;  
6 LLFCLVTPPSCVLSQVQLKQSGPGLVQPQSLSITCTVSGFSLTYSYGVHWVRQSPGKGL 65  
6 IFLLLSVTAGVHSGVQLQSGAELARPGASVKMSCKASGYTFYTRTMHWVKRPGQGLE 65  
66 WLGI-V-WSGGDTDNAAFISSLISKONSKSOLPFKMSLRATDTAIYVCARNRGGDIYD 124  
66 WIGYNPSRGVNTNPKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVIYCAR-----YYD 120  
125 FTYAMDYWGQGTSTVTSVSAKTTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPPESVTVTN 184  
121 DRYCLDYWGQGTSTVTSVSAKTTAPSVYPLAPVCGDGTGSSVTLGCLVKGYPPVPTLTWN 180  
185 SGSLSSSVHTFPALQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKLEPSPG 244  
181 SGSLSSSVHTFPALQSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKLEPSPG 240  
245 ISTINPCPCKECHKCAPNLEGSPSVFIFPPNIDKVLMSITLTPKVTGVVDVSDDDPDV 304  
241 --TIKPCPC-----KCAPNLLGGSPVFIFPPNIDKVLMSITLTPKVTGVVDVSDDDPDV 294  
305 QISWFWNNVEVHTAQTQTHREDYNSITIRVWSTLPIQHDQMSGKEFKCKVNNKDLPSPIE 364  
295 QISWFWNNVEVHTAQTQTHREDYNSITIRVWSTLPIQHDQMSGKEFKCKVNNKDLPSPIE 354  
365 RTISKIKGLVRAPQVYVILPPPAEQLSRKDVSLTCLVGVGNPGDISVWTSNGHTEENYKD 424  
355 RTISKPKGSVRAPQVYVILPPPEEEMTKQVLTLCVMTDFMPEDIIYVETNNGKTELNYKN 414  
425 TAPVLDSGSGFYIYKLNKMTSKWEKTSFSCNVRHGLKNYLYLKKTISRSPGK 478  
415 TEPVLDSGSGFYIYKLNKMTSKWEKTSFSCNVRHGLKNYLYLKKTISRSPGK 468

RESULT 3

US-08-397-411-7  
Sequence 7, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 61.9%; Score 1580.5; DB 3; Length 446;  
Best Local Similarity 64.6%; Pred. No. 1.5e-118;  
Matches 297; Conservative 63; Mismatches 85; Indels 15; Gaps 4;

QY 20 QVQLKQSGFGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKLEWLGVIWGGGDTDN 79  
DB 1 QVQLKQSGFGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKLEWLGVIWGGGSTEIN 60  
QY 80 AAFISRLTSKDNKSKQLFFKMNLSRATDTAIYYCARNRGDIYYFTYAMDYWGQGTSTV 139  
DB 61 AAFISRLTSKDNKSKQLFFKMNLSRATDTAIYYCARNRGDIYYFTYAMDYWGQGTSTV 113  
QY 140 VSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPESVTVTNWSSGSLSSSVHTFPALL 199  
DB 114 VSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPESVTVTNWSSGSLSSSVHTFPALL 199  
QY 173 VSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPESVTVTNWSSGSLSSSVHTFPALL 173  
QY 200 Q-SGLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVVDKLEPSGPISTINPCPCCKECH 258  
DB 174 QSSGLYSSSVTPSPSTWPSOTVTCVAHPASSTVVDKLEPSGPISTINPCPCCKECH 227  
QY 259 KCPAPNLEGGPSVFIFPPNPKIKDLVMSLTPTVVDVSDPDVQISWFFVNNVEVHTA 318  
DB 228 -CPAPNLEGGPSVFIFPPNPKIKDLVMSLTPTVVDVSDPDVQISWFFVNNVEVHTA 286  
QY 319 QTQTHREDYNTIRVSTPLTOHODWMSGKFEKCKVNNKDLPSPIERTISKIGLVRAPO 378  
DB 287 KTKPREQYNTYRVSVLTPLTOHODWMSGKFEKCKVNNKDLPSPIERTISKIGLVRAPO 346  
QY 379 VYILPPAPAEOLSRKDVSLTCLVGFNPGDISVETSNHGTENKDTAPVLDSDGSYFIY 438  
DB 347 VYILPPAPAEOLSRKDVSLTCLVGFNPGDISVETSNHGTENKDTAPVLDSDGSYFIY 406  
QY 439 SKLNMTSKWEKTSFSCNVRHEGLKNYLKKTSRSPGK 478  
DB 407 SKLTVDKSRQOGNVSFSCNVRHEGLKNYLKKTSRSPGK 446

## RESULT 4

Sequence 36, Application US/08353400  
Patent No. 5665357

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-36

Query Match 59.4%; Score 1515; DB 1; Length 464;  
Best Local Similarity 60.3%; Pred. No. 2.7e-113;  
Matches 286; Conservative 72; Mismatches 100; Indels 16; Gaps 6;

QY 6 LFLCLVTFPSCVLSQVQLKQSGFGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKLE 65  
DB 6 LILFLVATGTDVHSQVQLKQSGFGLVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKLE 65  
QY 66 WLQ-VIWSGGDIDYNAAFISRLTSKDNKSKQLFFKMNLSRATDTAIYYCARNRGDIYD 124  
DB 66 WIGEVNPTSGRSDYNEKFKKATLTVDKSTTAYMQLSSLTSDSAVYICARERA---YG 122  
QY 125 FTVAMDYWGQGTSTVTVSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPESVTVTN 184  
DB 123 YDDAMDYWGQGTSTVTVSSAKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYPESVTVTN 182  
QY 185 SGLSSSVHTFPALLOSLQSLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVVDKLEPSGP 244  
DB 183 SGLSSSVHTFPALLOSLQSLYTMSSSVTPSPSTWPSOTVTCVAHPASSTVVDKLEPSGP 239  
QY 245 ISTINPCPCCKECHKCPAPNLEGGPSVFIFPPNPKIKDLVMSLTPTVVDVSDPDV 304  
DB 240 ----RDC-GCKPC-ICTVPEVS---SVFIFPPKPKDVLITLTPKTCVVDISKDDPEV 290  
QY 305 QISWFFVNNVEVHTAQTQTHREDYNTIRVSTPLTOHODWMSGKFEKCKVNNKDLPSPI 364  
DB 291 QFSWVDDVEVHTAQTQTHREDYNTIRVSTPLTOHODWMSGKFEKCKVNNKDLPSPI 350  
QY 365 RTISKIGLVRAPOVYILPPAPAEOLSRKDVSLTCLVGFNPGDISVETSNHGTENKDY 424  
DB 351 RTISKIGLVRAPOVYILPPAPAEOLSRKDVSLTCLVGFNPGDISVETSNHGTENKDY 410  
QY 425 TAPVLDSDGSYFIYSKLNMTSKWEKTSFSCNVRHEGLKNYLKKTSRSPGK 478  
DB 411 TQPMINDTGSFVYSKLVNQSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK 464

## RESULT 5

US-08-353-400-33  
Sequence 33, Application US/08353400  
Patent No. 5665357

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

ATTORNEY/AGENCY AND ORIGINATOR:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1750

APPLICATION NUMBER: US/08/765,469  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/267,641  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1750  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 599 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-765-469-18

Query Match 58.2%; Score 1484; DB 3; Length 599;  
Best Local Similarity 60.5%; Pred. No. 1.le-110;  
Matches 282; Conservative 70; Mismatches 90; Indels 24; Gaps 8;  
18 LSOVLKSGGLVOPQSLSITCTVSGFSLTSYGVHVRQSPGKGLWGVWSGGD-- 75  
153 LEQVLKSGGLVOPKGLSKLSCAASGFTFNFAWVRQAPGKGLWVARIRSKSNY 212  
76 -TDYNAAFISRLISIKNSKSKOLFPMKNSLRATDTAIYVCARNRGDIYDFYANDYWGQ 134  
213 ATSYGDSVKDRFTVSRRDSQSFMFLQMNKLTEDTAMTYCVR----VYVG---ANDYWGQ 265  
135 GTSVTVSAAKTPPSPVYPLAPCGDPT--TGSSVTLGCLVKGYPFSPSVTVMNSGSLSSV 192  
266 GTSVTVSAAKTPPSPVYPLAPCGSAAQTNMTVTLGCLVKGYPFSPSVTVMNSGSLSSV 325  
193 HTFAPALQSLGTYMSSSVTVSPSSVTPSTVCSVAHPASSTTVDKKLPSPGPISTINPCP 252  
326 HTFAPALQSLGTYMSSSVTVSPSSVTPSTVCSVAHPASSTTVDKKLPSPGPISTINPCP 377  
253 PKCKECHKPAPNLEGGPSPVFPPNPKDVLMLSLTPKVTCTVVDVSEDDPDVQISWVNN 312  
378 GCKPC-ICTVPEVS---SVFIFFPKPKDVLITLTPKVTCTVVDVSEDDPDVQISWVNN 433  
313 VEVHTAQTHREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKTG 372  
434 VEVHTAQTHREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKTG 493  
373 LVRAQVYILPPRAQVLSRKDVSTLCLVGVNPGDISVWETSNGHTEENYKDTAPVLDS 432  
494 RPKAPQVYILPPRAQVLSRKDVSTLCLVGVNPGDISVWETSNGHTEENYKDTAPVLDS 553  
433 GSYFIYSLKLNKTSKWEKTSDFSCNVRHEGLNKKYLLKKTISRSPGK 478  
554 GSYFVYSLKLNKTSKWEKTSDFSCNVRHEGLNKKYLLKKTISRSPGK 599

RESULT 8

US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCTUT01  
CLONE: 1513264  
US-09-049-672A-4

Query Match 57.7%; Score 1471.5; DB 4; Length 473;  
Best Local Similarity 58.8%; Pred. No. 8.2e-110;  
Matches 285; Conservative 70; Mismatches 111; Indels 19; Gaps 6;

QY 1 MAVLLGLFCLVFPSCVLSOVOLKSGGLVOPQSLSITCTVSGFSLTSYGVH--WVRQ 58  
Db 1 MKHLFFLLVAAAPRWVLSQVQLQESGGLVAPSETLSLTCAVSGGSIISGYYSWIRQ 60  
QY 59 SPKGLEWLVGIVWSGGDTYNAAFISRLISIKNSKSKOLFPMKNSLRATDTAIYVCARN- 117  
Db 61 PPGKLEWLVGIVWSGGDTYNAAFISRLISIKNSKSKOLFPMKNSLRATDTAIYVCARN- 120  
QY 118 ---RGDIYDFYANDYWGQGTSTVSSAKTTPPSPVYPLAPCGDPTTGSSVTLGCLVKG 174  
Db 121 VGLRGG----NYGMDVWGQGTSTVSSAKTTPPSPVYPLAPCGDPTTGSSVTLGCLVKG 175  
QY 175 FPESVTVTNWSSGSLSSVHTPALLO--SGLYTMSSSVTVSPSSVTPSTVCSVAHPASST 233  
Db 176 FPEPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVSPSSVTPSTVCSVAHPASST 235  
QY 234 TVDKKLEPSGPISTINPCPCCKECHKPAPNLEGGPSPVFPPNPKDVLMLSLTPKVTCTV 293  
Db 236 KVDKRVPEKSCDKT-HTCPC-----CPAPLLEGGPSPVFPPNPKDVLMLSLTPKVTCTV 288  
QY 294 VVDVSEDDPDVQISWVNNVEVHTAQTHREDYNSTIRVSTLPIQHDWMSGKEFKCK 353  
Db 289 VVDVSHEDPEVKFNWYVGVHNAKTPREQNSTYRVSVTLVLDHQLWLNKKEYCK 348  
QY 354 VNNKDLPSPIERTISKTGKLVRAQVYILPPAPQLSRKDVSLCLVGVNPGDISVWET 413  
Db 349 VSNKALPAPIERTISKAKGQPREQVYILPPSPREMTKNQVSLCLVKGFTPSDIADVWE 408  
QY 414 SNGHTEENYKDTAPVLDSGDSYFIYSLKLNKTSKWEKTSDFSCNVRHEGLNKKYLLKKTIS 473  
Db 409 SNGOPNNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHTYQKSL 468  
QY 474 RSPGK 478





199 LO-SGLYTMSSSVTPSPSTWPSOTVCSVAHPASSTVVDKLLPSGPISTINPCPPCKEC 257  
179 LQSSGLYSLSSVTPSPSSLTGTQYICNVNHPKNTKVDKKVEPKSCDKT-HTCPEP----- 233  
258 HKCPAPNLEGGSPVFIFPPNKKVIMSLTPKVTCTVVVDVSDDDPQVQISWVFNNEVHT 317  
234 --CPAPPELLGGSPVFLPPKPKDPLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVHN 291  
318 AQOTQTHREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377  
292 AKTPREEQYNSTIRVSVTLVHLQDNLNGKEYCKVSNKALPAPIERTISKAKGQPREP 351  
378 QVYTLPPAPLQSLSKDYSCLVCLVGFNPGDISVETWTSNGHTEENYKDTAPVLDSDGSYFI 437  
352 QVYTLPPSREEMTKNQVSLTCLVKGFPSPDIADVEWESNGQPPENYKTPPPVLDSDGSFFL 411  
438 YSKLNMKTSKWEKTDSPSCNVRHGLKNYLLKTKTISRSPGK 478  
412 YSKLTVDKSRWQOGNVFSCSVNHEALHNHYTKQKLSLSLSPGK 452

## RESULT 13

-09-234-340A-71

Sequence 71, Application US/09234340A

Patent No. 6468532

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokhi, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/234,340A  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,952  
FILING DATE: 24-Jul-1998  
APPLICATION NUMBER: 60/074330  
FILING DATE: 22-JAN-1998

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/075467  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881

## INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

Query Match 57.18; Score 1456.5; DB 4; Length 452;  
Best Local Similarity 60.18; Pred. No. 1.2e-108;  
Matches 277; Conservative 68; Mismatches 105; Indels 11; Gaps 5;

QY 20 QVQLKQSGPGLVQPSSQSLSTICTVSGFSLTSGYVHVHQRSPGKLEWLGVI--WSGGDTDY 78  
Db 1 EVQLVQSGGGLVQPSSGLRLSCAASGYFSFHHYHWRQAPGKLEWVGIDPSNGETTY 60  
QY 79 NAAFIISRLSISKDKNSKQLFFKMNLSLRATDTAIYYCARNRGGDIYYDFYAMDYNGQGTSV 138  
Db 61 NQKFKGRFTLSRDNSKNTAYLQMNSLRADDTAVYYCA--RGDIRYNGDFWDFVWGQGTFLV 118  
QY 139 TVSSAKTTPPSVYPLAPCGGDTTSGSVTLGLVKGYPPESTVTVNWSGLSSSVHTFPAL 198  
Db 119 TVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNNSGALTSGVHTFPV 178  
QY 199 LQ-SGLYTMSSSVTPSPSTWPSOTVCSVAHPASSTVVDKLLPSGPISTINPCPPCKEC 257  
Db 179 LQSSGLYSLSSVTPSPSSLTGTQYICNVNHPKNTKVDKKVEPKSCDKT-HTCPEP----- 233  
QY 258 HKCPAPNLEGGSPVFIFPPNKKVIMSLTPKVTCTVVVDVSDDDPQVQISWVFNNEVHT 317  
Db 234 --CPAPPELLGGSPVFLPPKPKDPLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVHN 291  
QY 318 AQOTQTHREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377  
Db 292 AKTPREEQYNSTIRVSVTLVHLQDNLNGKEYCKVSNKALPAPIERTISKAKGQPREP 351  
QY 378 QVYTLPPAPLQSLSKDYSCLVCLVGFNPGDISVETWTSNGHTEENYKDTAPVLDSDGSYFI 437  
Db 352 QVYTLPPSREEMTKNQVSLTCLVKGFPSPDIADVEWESNGQPPENYKTPPPVLDSDGSFFL 411  
QY 438 YSKLNMKTSKWEKTDSPSCNVRHGLKNYLLKTKTISRSPGK 478  
Db 412 YSKLTVDKSRWQOGNVFSCSVNHEALHNHYTKQKLSLSLSPGK 452

## RESULT 14

US-08-487-550-12

; Sequence 12, Application US/08487550

; Patent No. 6113898

## GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

## CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314

## COMPUTER READABLE FORM:

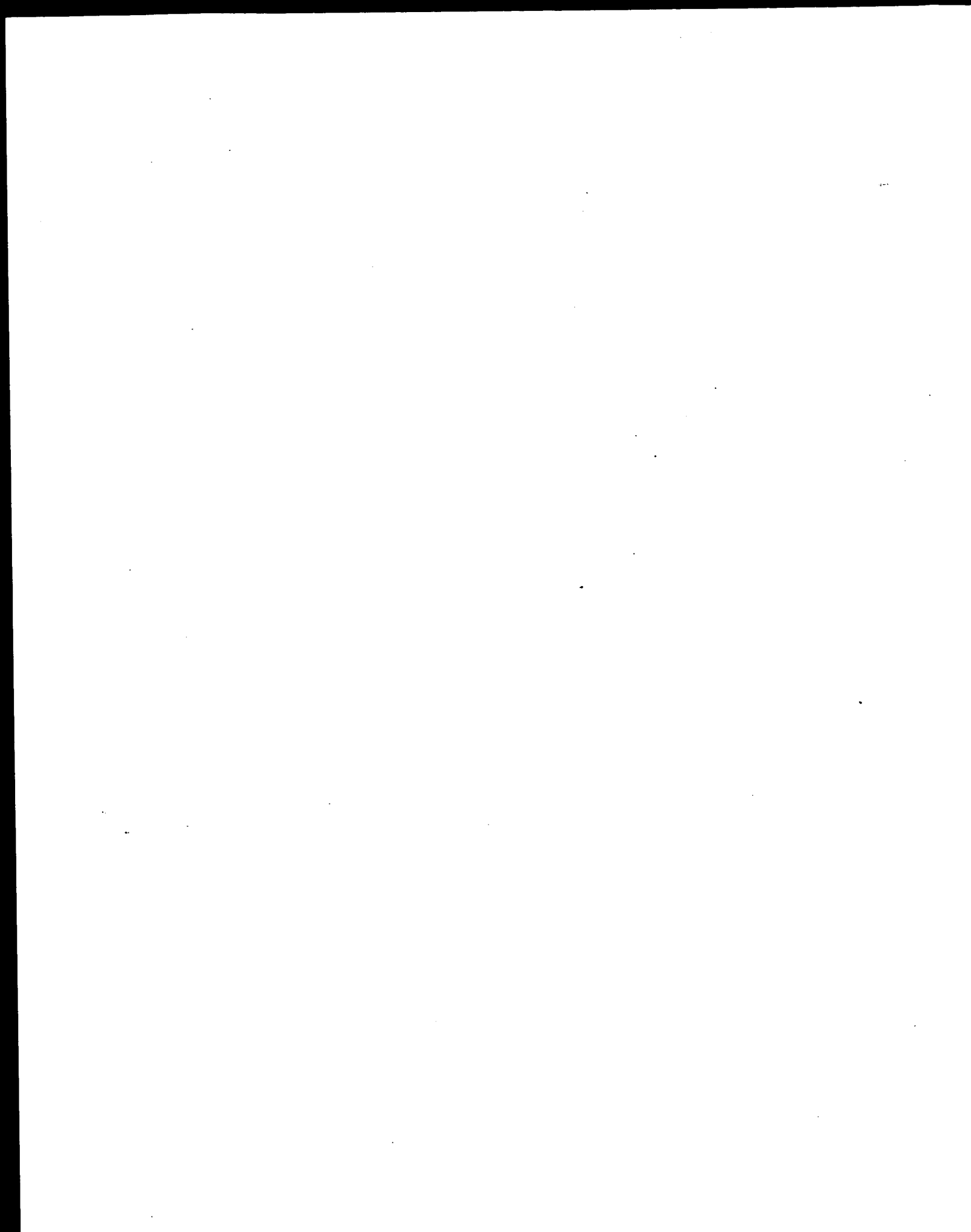
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,550  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:



Search completed: June 18, 2003, 16:49:18  
Job time : 25.4972 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:53 ; Search time 65.7921 Seconds  
(without alignments)  
968.107 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLLCLVTFPSCVLSQ.....RHEGLKNYKLTISRSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A\_Geneseq\_101002:\*

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*

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19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	2083.5	81.6	454	23	AB76124
2	2083.5	81.6	462	23	AB76126
3	1789.5	70.1	341	9	AA93200
4	1751	68.6	468	12	AA13061
5	1727.5	67.7	469	14	AA40384
6	1711	67.0	477	15	AA47450
7	1669	65.4	447	10	AA93037
8	1596	62.5	476	22	AA49243
9	1565.5	61.3	446	17	AAW05829
10	1554.5	60.9	581	22	AA81972

11	1515	59.4	464	16	AA76088
12	1502	58.9	445	16	AA76085
13	1497.5	58.7	464	23	AAU72801
14	1493.5	58.5	465	16	AA66958
15	1484	58.2	599	17	AA90837
16	1480.5	58.0	448	14	AA43673
17	1479.5	58.0	448	17	AA97376
18	1472	57.7	456	23	AA18370
19	1472	57.7	464	19	AAW83041
20	1472	57.7	464	21	AA814747
21	1472	57.7	484	21	AA90897
22	1472	57.7	464	23	AB74866
23	1472	57.7	464	23	AB74912
24	1471.5	57.7	473	22	AB36206
25	1470.5	57.6	448	17	AA99843
26	1459.5	57.2	477	22	AAU14288
27	1458	57.1	451	21	AA93734
28	1456.5	57.1	448	11	AA06476
29	1456.5	57.1	452	20	AA29458
30	1456.5	57.1	452	21	AB30322
31	1456.5	57.1	452	21	AA77766
32	1456	57.1	461	14	AA44494
33	1454.5	57.0	452	19	AAW69316
34	1452.5	56.9	551	22	AB56471
35	1450.5	56.8	466	5	AA40032
36	1448.5	56.8	475	17	AA93353
37	1447	56.7	475	13	AA20057
38	1445	56.6	476	18	AAW01822
39	1445	56.6	476	19	AAW63765
40	1445	56.6	476	23	AAU11646
41	1440	56.4	451	22	AAE12715
42	1439.5	56.4	475	18	AAW11641
43	1439.5	56.4	519	23	AAU81993
44	1434.5	56.2	475	18	AAW11639
45	1433	56.2	470	13	AA22757

## ALIGNMENTS

RESULT 1

AB76124

ID AB76124 standard; Protein; 454 AA.

XX

AC AB76124;

XX

DT 15-JUL-2002 (first.entry)

XX

DE Recombinant 4G10 antibody heavy chain.

XX

KW Monoclonal antibody; antibody; 4G10; phosphotyrosine; cancer; diagnosis.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 5

FT /note= "encoded by CAR"

XX

PN WO200218443-A2.

XX

PD 07-MAR-2002.

XX

PF 30-AUG-2001; 2001WO-US26926.

XX

PR 01-SEP-2000; 2000US-0653755.

XX

PA (UPST-) UPSTATE BIOTECHNOLOGY INC.

XX

PI Esinger D, Stiles L, Lamarche A, Jelinek T;

XX

DR WPI; 2002-393728/42.

DR N-PSDB; ABL56966.

1

QY  
318 32101

**PSP TSK I K L V R A P 37**

W dia



$$I = \text{rate} \times \text{constant} / \text{rate} + \text{constant}$$

**F**

Db 370 VYVLPPEEMTKKQVTLTCMTDFMPEDIYVWNTNGKTELNYKNTPEVLDSGSGYFW 429

QY 439 SKLNKTKSWEKTDGFSFCNVRHEGLKNYLLKTTISRSPGK 478

Db 430 SKLRVEKNWVERNSYSCSVHGLHNHHTTKSFSTPGK 469

RESULT 6

AAAR47450

ID AAR47450 standard; Protein; 477 AA.

AC AAR47450;

XX

24-JUN-1994 (first entry)

XX

DE T84.12 Heavy chain.

XX

Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;

KW region; transmembrane; myeloma cell; light chain; tumour.

XX Synthetic.

JS

XX

W09325237-A.

PN

23-DEC-1993.

XX

15-JUN-1993; 93WO-US05709.

XX

15-JUN-1992; 92US-0904074.

XX

(CITY ) CITY OF HOPE.

XX (YANG/) YANG Y.

XX

Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;

XX Yang YH;

XX

WPI; 1994-007204/01.

XX N-PSDB; AAQ54652.

XX

New chimeric T84.12 antibody active against carcinoembryonic

T antigen - has murine variable and human constant regions, also

T DNA encoding it and transformed myeloma cells

XX

Claim 1; Page 17; 27pp; English.

XX

The sequences (AAQ54651-52) show the light and heavy chain cDNAs

XX of murine T84.12. The T84.12 antibody is directed against the

XX tumour marker carcinoma embryonic antigen, and is useful for

XX tumour imaging and immunotherapy.

C The amino acid sequence given in the specification has been

C incorrectly identified as a nucleic acid sequence, therefore

C unacceptable characters have been represented as an 'N'.

C The amino acid sequence given below has been derived from the

C cDNA, by the indexer.

XX

Q Sequence 477 AA;

Y Query Match 57.0%; Score 1711; DB 15; Length 477;

b Best Local Similarity 59.1%; Pred. No. 2e-103;

Matches 326; Conservative 53; Mismatches 83; Indels 10; Gaps 3;

7 LFLCLVTFPSCVLSQVQLKSGDGLVPSQSLSTCTVSGFSLTSYGVHWVRQSPGKLEW 66

16 LFLVLVLKGVQCEVKLVESGGGFVPGGSLKLSCAAGFTFSSYAMSVWRQTPKRLW 75

67 LGVWISGGDPTDYNAAIFSLRLSISKDNSKQLFPMKNSLRATDTAIYICARNRGDIYDFT 126

76 VASISSDGIITFYVDVSVKGRFTVSRDNRARILYLQMSLSRSEDATMYICAR----IDYGG 131

127 YAMDYWGQCTSVTVSSAKTTPPSVYPLAPGCGDTGSSVTGLCLVKGYPPESVTWNWG 186

132 GGFYWGQGTATVSAKATAPASVPLAPVCGDTGSSVTGLCLVKGYPPPEPTLWNWG 191

QY 187 SLSSSVHTPALQSLGYTMSSSVTPSPSTWPSQTVTCSVAHPASSTTVDKKLEPSPIS 246

Db 192 SLSSGVHTFPVQLQSDLYTLSSSVTVTSSWPSQITCNVAHPASSTKVDKKTIEPRGP-- 249

QY 247 TINPCPCKECHKCAPNLEGSPSVIFPPNPKVDLMISLTPKVTVCVVVDVSEDDPDVQI 306

Db 250 TIKPCPCP-----KCPAPNLIGGSPSVIFPPNPKVDLMISLTPKVTVCVVVDVSEDDPDVQI 305

QY 307 SWFVNNVEVHTAQTHREDYNSTIRVSTLPIQHODMWSGKEFKCKVNNKDLPSPIERT 366

Db 306 SWFVNNVEVHTAQTHREDYNSTLRVSAALPIQHODMWSGKEFKCKVNNKDLPSPIERT 365

QY 367 ISKIKGLVRAPQVYILPPPAEQLSRDKDVSITCLVGVFNPGDISVEMTSGHTEENYKDTA 426

Db 366 ISKPKGSVRAPQVYILPPPEEEMTKQVTLTCMTDFMPEDIYVWNTNGKTELNTKANTE 425

QY 427 PVLDSGSGYFIYSKLMNMTSKWEKTDGFSFCNVRHEGLKNYLLKTTISRSPGK 478

Db 426 PVLDSGSGYFMYSKLRVEKNWVERNSYSCSVHGLHNHHTTKSFSTPGK 477

RESULT 7

AAAP93037

ID AAP93037 standard; protein; 447 AA.

XX

AC AAP93037;

XX

14-MAR-1990 (first entry)

XX

Chimeric antibody heavy chain variable region.

XX

Mus.

XX

KSL/4; chimeric antibody; heavy chain variable region;

XX

EP338767-A.

PN

25-APR-1989.

XX

18-APR-1989; 89EP-0303814.

XX

21-APR-1988; 88US-0184522.

XX

(ELIL ) ELI LILLY AND CO.

XX

Beavers LS, Bumol TF, Gadski RA, Weigel BJ;

XX

WPI; 1989-311203/43.

XX N-PSDB; AAN91659.

XX

Recombinant DNA cpds. producing antibodies - monoclonal and

PT chimeric derived from monoclonal antibody KSL/4.

XX

Claim 6; page 50; 89pp; English.

XX

The sequence encodes the heavy chain of MAb KSL/4, used to

CC construct mouse/human chimeric antibodies. KSL/4 is a murine antibody

CC which binds to surface antigens on adenocarcinoma cells and the use of

CC human C regions avoids immunological problems during treatment.

XX

Q Sequence 447 AA;

Y Query Match 65.4%; Score 1669; DB 10; Length 447;

b Best Local Similarity 68.5%; Pred. No. 1e-100;

Matches 317; Conservative 52; Mismatches 74; Indels 20; Gaps 6;

20 QVOLKSGGGLVOPQSLSITCTVSGFSLTSYGVHWVRQSPGKLEWLVWISG---GDT 76

1 QIQLVSGGPELKPGETVKISCRASGYFTNYGMNWKQTPGKGLKWMG--WINTYTGP 58

77 DYNAAFISRLSISKDNSKQLFPMKNSLRATDT-AIYICARNRGDIYDFTYAMDYWGQ 135

Db 59 TYADDFKGRFAFSLTASATAFLQIQPQNRMTATYFCVR-----FISKGDYWGQ 110

```

136  TSVTVSSAKTTPPSVYPLAPGCGDPTGSSVTLGCLVKYGFPESTVTVWNSGSLSSSVHTE 195
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
111  TSVTVSSAKTTAPSVYPLAPGCGDPTGSSVTLGCLVKYGFPEPTVLWNSGSLSSGVHTF 170
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
196  PALLQSGLYTSSSVTVFSSWTWPSQTVC7SAHPASSSTTVDKLEPSPGISTINPCPPCK 255
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
171  PAVLQSDLYTLSSSVTVSTWPSQITCNVAHPASSTKVKDKTEPRGP--TIKPCPPC- 227
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
256  ECHKCAPNLEGGPSVFIFFPNNIKOVLMISLTPKVTGVVDVSEDDPDVQJISWFVNVEV 315
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
228  ---KCAPNLLGGPSVFIFFPKIKOVLMISLPIVTVVDVSEDDPDVQJISWFVNVEV 284
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
316  HTAQOTQTHREDYNSTIRVVYSTLPIQHDWMSGKEFKCKVKNKNDLPSPETERISIKIGLVR 375
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
285  HTAQOTQTHREDYNSTLRVVVSALPIQHDWMSGKEFKCKVKNKNDLPAPLERTISPKGSVR 344
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
376  APOVYTLPPAQLSKDVSL7CLVVGFPNGDISVEMTSNGHTEENYKDTAPVLDSGYS 435
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
345  APOVYVLPPEEMTFKQVTL7CMVTDPMPEDIYVETWNGCKTELNYKTEPVLDSGYS 404
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
436  FIYSKLNMKTSKWEKTD7SFSCNVRHEGLKNYLYKKTISRPOK 478
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
105  FMYKTL7PVEKKNVWRNYS7SCSVQOEGHNNHHTTKSFSTPKQ 447
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

2243 standard; protein; 476 AA.  
2243;  
AR-2001 (first entry)  
eric 4H6 anti-DR4 antibody heavy chain protein.  
Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;  
immune.

[illegible]

RESULT	9
AAW05829	
ID	AAW05829 standard; Protein; 446 AA.
XX	
AC	AAW05829;
DD	27-JAN-1997 (first entry)
XX	
DE,	Humanised 1D10 antibody heavy chain.
XX	
KW	B-cell lymphoma; humanised antibody; bis-
KW	myeloma; leukaemia; hybridoma; monoclonal
XX	
OS	Chimeric Homo sapiens; .
OS	Chimeric Mus sp.
XX	
FH	Key Location/Qualifiers
FT	Domain 1..116
FT	/label= Variable_domain
FT	Region 31..35
FT	/label= CDR1
FT	Region 50..65
FT	/label= CDR2
FT	Region 98..105
FT	/label= CDR3
FT	Domain 117..214
FT	/label= CH1
FT	Domain 215..229
FT	/label= Hinge
FT	Domain 230..339
FT	/label= CH2
FT	Domain 340..446
FT	/label= CH3
XX	
NN	WO9626964-A1.

Query Match	62.5%;	Score 1596;	DB 22;	Length 476;
Best Local Similarity	63.8%;	Pred. No. 6.1e-96;		
Matches 305. Conservative	65;	Mismatches 96;		
Indels	12;	Gaps	4;	



01-MAR-1995; 95US-0397411.  
(IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.  
(PROT-) PROTEIN DESIGN LABS INC.  
Gingrich R, Link BK, Tso JY, Weiner G;  
WPI; 1996-412742/41.  
New bispecific antibody reactive with both T or NK cells and  
malignant B cells - also their humanised forms and hybridomas  
producing them, useful for treating or preventing leukaemia,  
lymphoma and myeloma  
Example 4; Fig 4e; 85pp; English.  
The humanised ID10 antibody heavy chain (AAW05829) includes a  
variable region (see also AAW05823) consisting of human R3.5HG heavy  
chain variable region framework and complementarity determining  
regions from the murine ID10 antibody specific for a 28/32 kDa  
antigen found on the surface of malignant B-cells. It can be  
coexpressed with humanised ID10 light chain (see also AAW05828) in  
mammalian host cells. Bispecific antibodies can be constructed that  
include a first binding fragment comprising humanised M291 heavy and  
light chain variable regions (see also AAW05826, AAW05830), and a second  
binding fragment comprising humanised ID10 heavy and light chain  
variable regions. Such antibodies are reactive with both T or NK  
cells and malignant B cells, and have therapeutic and diagnostic  
appls.

Sequence 446 AA;

Query Match 61.3%; Score 1565.5; DB 17; Length 446;  
Best\_Local Similarity 64.1%; Pred. No. 5.5e-94;  
Matches 295; Conservative 63; Mismatches 87; Indels 15; Gaps 4;

**y**

20 QVQLKQSGPGLVPQSLSITCTVS6SFSLTSGYHHWRQQSPGKGLEWLGVTWSGGDTYN 79  
| | | | : : : : | : | : | : | : | : | : | : | : | : | : |  
**b** 1 QVQLQESGPGLVKPSSETISLTCTVS6SFLTYGYHWRQQSPGKGLEWIGKVWGSGSTEYN 60  
| | | | : : : : | : | : | : | : | : | : | : | : | : | :

80 AAFISRLTSKDNKSQLEFFKNLSLRATDTAIYYCARNRGDIYYDFYAMDYWGQGSVTV 139  
|||||:|||||: :||| :|||:||||| :||||| :|||  
61 AAFISRLTSKDTSKNQVLSKLNSTAAATVYYCARND-----RYAMDYWGQGLTVT 113

140 VSSAKTTPSYVPLAPCGDITGSSVTLCGLVKGFPESVTVTVNNSGSLSSSVHTFPALL 199  
 |||| | |||:|||| | : ||||| |||| |||:|||| | |||:|  
 114 VSSATKGPSEVPLAPSSKSTSGGTAALCGLVKVDFPEPTVTVNNSGALTSGVHFTPAVL 173

200 Q-SGLYTMSSVYVPSPWPSQVTCVSHAHPASSTVVDKLEPSPISTINPCPPCKECH 258  
 + |||||::|| |||||:: || ||| ||| |||||:: ||| + ||||  
 174 QSSGLYLSVVYVPSPSLGQTICNVHNPSTKVDKVEPKSCDKT-HTCPP----- 227

259 KCPAPNLEGGSVTFPPNNIKDVLMSLTPKVTCCVVVDSEDDPDQISWFFVNNVEHTA 318  
||||| |||||:||||| || |||||:||||| |||||:||||| |||||:|||||

228 -CPAPELLGGSVTFPPPKPDKDTLMISRTPEVTCCVVVDVSHEDPEVKFNKYVDGVEVHNA 286

319 QTQTHREDYNTIRWSTLPQHODWSGKEFKCVNNKDLPSPIERTISKIGLVRAPQ 378  
:: | ||| |||| : ||||:::||||:| |:::||:|||| |  
287 KTKPREEDYNTYRWSVLTVLHODWLNGEYKCVSNKALPAIEKTISKAGOPREPO 346

379 VYIIPPAQLSRKDVSLTCLVGFNPGDISVEWTSGHTEENYKDTAPVLDSGVSFFIY 438  
||| | : || : ||| | | | | | | | | | | | | | | | |  
347 VYTTPPSDELTKNQVSLTCLVGFYPSDIAVESNGOPENNYKTTVPVILDSGVSFFIY 406

```

439 SKLNNKTSKVEKTDFSCNVRHEGLKNYYLKTKTISRPGK 478
    ||| : !:!: :: |||| | | | : | : | | |
407 SKLTVDKSQQQGNVFCSYMHAEALHNHYTKLSISLSPGK 446

```

RESULT 10  
AB81972

0 AAB81972 standard; Protein; 581 AA.

Downloaded from <http://ajph.org/> on November 10, 2014

XX	AAB81972;	
XX		
DT	03-JUL-2001 (first entry)	
XX		
DE	Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.	
XX		
KW	Ganglioside; GD2; complementation determining region; CDR; antibody;	
KW	mouse; cancer.	
XX		
OS	Synthetic.	
XX		
PN	WO200123573-A1.	
XX		
PD	05-APR-2001.	
XX		
PF	29-SEP-2000; 2000WO-JP06773.	
XX		
PR	30-SEP-1999; 99JP-0278290.	
XX		
PA	(KYOW ) KYOWA HAKKO KOGYO KK.	
XX		
PI	Hanai N, Shitara K, Nakamura K, Niwa R;	
XX		
DR	WPI; 2001-266163/27.	
XX		
PT	Human type complementation-determining domain transplanted-antibody and	
PT	derivatives against ganglioside GD2, useful in diagnosis and therapy of	
PT	e.g. tumours, has low antigenicity, little side effects but potent	
PT	activity in cancer	
XX		
PS	Example 3; Page 111-114; 123pp; Japanese.	
XX		
CC	The present invention describes an antibody, which can react specifically	
CC	with ganglioside GD2, and is transplanted with a human type	
CC	complementation-determining domain (CDR), or its fragments. The antibody	
CC	and its derivatives are useful in diagnosis and therapy of tumours,	
CC	particularly cancer diagnosis. The present sequence is a protein	
CC	used in the exemplification of the invention.	
XX		

Sequence 581 AA;

Query Match 60.9%; Score 1554.5; DB 22; Length 581;  
Best Local Similarity 63.9%; Pred. No. 3.8e-93;  
Matches 294; Conservative 64; Mismatches 89; Indels 13; Gaps 5;

Qy	20	QVQLKSGPGLVPQSLSITCTVSGFSLTISYGVHWYRQSPGKLEWLVINWGSDTDYN	79
		:     :     :     :     :     :     :     :	
Dd	1	QVQLQESGPGLVKPSQTLSTCTVSGFLSYNIHWYRQPPGKLEWLVINWGGSNYN	60

QY	80	A A F I S R L S I S K D N S K S O L F P K M S L R A T D T A I Y C A R N R G D I Y D F T Y A M D Y W Q G Q S V T	139
Db	61	S A L M S R L T I S K D N S K N Q V F L K M S L R A A D T A V Y C A K - R S D D I S W F A - - - - W Q G G T L V T	115

QY	140	VSSAKTTPPSVYPLAPCGD	TTGSSVTLGCLVKGYFPESVTV	TWNSGSLSSSVHTFPALL	199
Db	116	VSSASTKGPSVFLAPSSKST	SGTALGCLVKDYPPETV	GSWNSGALISGVHTFPAVL	175

QY	200 Q-SGLVTMSSVTPSPSTWPSQTCSVAHPASSTTVDDKLESGPISTINCPCKECH	258
	:             :     :             :	
Db	176 QQSGLYSLSVVTPSSSGLGTQTYICNVNHNKPNTKVDDKKVEPKSCDKT-HTCpP-----	229

QY	259	KCPAPNLEGGSPVFIEPPNKKDVLMLSLTPKVT	318
		:     :      :     :      :	
D6	230	-CPAPELLGGSPVFLFPFKPKDTLMISRTPEVTCV	288
		:     :      :     :      :	

QY 319 QTCTHREYNSTRVVSUPLIOHQDMSCKEFCCKYNNKDLPSPIERTISKIKGLVRAPQ 378  
:  
Db 289 KTKPREEQNSTRYRVSVLTVIHDQNLNKYCKYSNRPALPAIEKTISKAKGPREPO 348

```

QY      379 VYLPPPAQLSRKDVSTCLVVGPNPGISVEWTSNGHTEENKYKTAPVLDSGVSFFI 438
        ||| |::: ||||| | |::| | |::| | |::| | |::| | |::| | |::| |
Db      349 VTLPSPRDELTKNVSTCLVKGYFPSIAVWEWSNGOPENNYKTPPVLDSGVSFFI 408

```

1000

\_\_\_\_\_



SQ	Sequence	445 AA;
Query Match	58.9%; Score 1502; DB 16; Length 445;	
Best Local Similarity	61.3%; Pred. No. 7.4e-90;	
Matches	282; Conservative 68; Mismatches 94; Indels 16; Gaps 6;	
QY	20 QVQLKSGGGLVQPSQSLSITCTVSGFSLTSYGVHVRQSPGKLEWLG-VIWSGGDTDY 78	
Db	1 QVQLQPGAEVLKPGASVQLSKASGTYTGTGWIHWVKRQPGQLEWIGVNFSTGRSDY 60	
QY	79 NAAFTSLRLSISKDNKSQQLFFKMSLRATDTALTYICARNRDIYDFTYAMDYWGQTSV 138	
Db	61 NEKFNKATLTVKSSSTTAYMQLSLSDTSASVYICARERA---YGYDDAMDYWGQTSV 117	
QY	139 TVSSAKTTPPSVYPLAPGCGDTGSGVTLCGLVKGVEPESVTVTWNSGSLSSVHTFPAL 198	
Db	118 TVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGTFPEPVTWNSGSLSSGVHTFPAP 177	
QY	199 LOSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVDKKLEPSPGISINPCPPCKECH 258	
Db	178 LOSGLYTLSSSVTVPSSTWPSQTCVNAHPASSTVKDKIYP-----RDC-GCKPC- 228	
QY	259 KCPAPNLGGGVSFFLPPNIDKVLMSLTPKVTCTVVDVSEDDPDVQISWFVNNVEHTA 318	
Db	229 ICTVPEVS---SVFIPFPKPKDKVLTITLPKVTCTVVDVSKDDPEVQFSWFVDDVEHTA 285	
QY	319 QTQTHREDYNSTIRVSTLPIQHDQWMSGKEFKCKVNNKOLPSPPIERTISKIGLVRAPQ 378	
Db	286 QTQPREQFNSTFRSVSELPIMHQDWLNGKEFKCKVNSAAPPAPPIERTISKIGRPAQ 345	
QY	379 VYILPPPAQLSKDKVSLTCLVGFNPGDISVEWTSNGHTENYKDTAPVLDSGYSFIY 438	
Db	346 VYTIPTPPKEQAKDKVSLTCLVGFNPGDISVEWTSNGHTENYKDTAPVLDSGYSFIY 405	
QY	439 SKLNKMSKWEKTSFSCNVNRHEGLKNYLLKKTISRSPGK 478	
Db	406 SKLVQKSNWEAGTFTCSVLHLEGLHNHHTKSLSHSPGK 445	
RESULT 13		
AAU72801		
D	AAU72801 standard; protein; 464 AA.	
C	AAU72801;	
X		
T	26-FEB-2002 (first entry)	
X		
E	TRA-8 heavy chain.	
X		
W	Tumour necrosis factor-related apoptosis-inducing ligand receptor;	
W	TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;	
W	autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;	
W	rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;	
W	Addison disease; scleroderma; Goodpasture's syndrome; sterility;	
W	myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;	
W	allergy; arteriosclerosis; myocarditis; cardiomyopathy;	
W	glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.	
X		
S	Mus musculus.	
X		
X	WO200183560-A1.	
X		
N	08-NOV-2001.	
D		
X	02-MAY-2001; 2001WO-US14151.	
F		
X	02-MAY-2000; 2000US-201344P.	
R		
X	(UABR-) UAB RES FOUND.	
X		
X	Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;	
I		
X	WPI; 2002-049338/06.	
R		
DR	N-PSDB; AAS97062.	
XX		
PT	Novel antibody specific for tumour necrosis factor-related	
PT	apoptosis-inducing ligand, useful for inhibiting cell proliferation in	
XX	cancer	
PS	Claim 26; Page 198-199; 229pp; English.	
XX		
CC	The invention describes a novel antibody which recognizes a tumour	
CC	necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor	
CC	DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing	
CC	activity to a cell expressing DR5 in vivo. It is also useful for	
CC	preparing a therapeutic for selective apoptosis of abnormal or	
CC	dysregulated cells, and for inhibiting cell proliferation in a cell,	
CC	preferably a human breast, ovary, colon, haematopoietic, prostate,	
CC	lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may	
CC	also be administered e.g. paclitaxel, taxol or cycloheximide. The	
CC	antibody is used to treat an autoimmune disease, systemic lupus	
CC	erythematosus, Hashimoto's disease, rheumatoid arthritis,	
CC	graft-versus-host disease, Sjogren's syndrome, Chron's disease,	
CC	pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,	
CC	autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple	
CC	sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,	
CC	allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,	
CC	glomerular nephritis, hypoplastic anaemia, rejection after organ	
CC	transplantation, and numerous malignancies of lung, prostate, liver,	
CC	ovary, lymphatic or breast tissue. Peptides used to design primers for	
CC	isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and	
CC	AAU72802), TRA-8 are shown in AAU72799 and AAU72800.	
XX		
SQ	Sequence 464 AA;	
Query Match	58.7%; Score 1497.5; DB 23; Length 464;	
Best Local Similarity	61.1%; Pred. No. 1.5e-89;	
Matches	291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;	
QY	4 LGLFCLVTFPSCVLSSQVQLKQSGFGLVQPSQSLSTCTVSGFSLTSYGVHVRQSPGK 63	
Db	5 LSLIF-LVILVLKGVQCEVNLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSVWQTPEKR 63	
QY	64 LEWLVGIVSGGD-TDYNAAFISRLSISKDNKSQLFKFNMSLRATDTALTYICARNRDIY 122	
Db	64 LEWVATISSGGSYTYVPDPSVKGRFTISRDNKNTLYLQMSLSRSEDYAMYCAR-RG--- 119	
QY	123 YDFIYAMDYWGQTSVTVSSAKTTPPSVYPLAPGCGDTTGGSVTLGCLVKGYPESVTVT 182	
Db	120 -DSMITTDYWGQGTTLTVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEVTVT 178	
QY	183 WNSGSLSSSVHTFPALQSLGTYMTSSSVTVPSSTWPSQTVCVAHPASSTTVDKKLEPS 242	
Db	179 WNSGSLSSGVHTFPALQSLDLYTLSSSVTVPSSTWPSQTCVNAHPASSTTKVKKIYP- 237	
QY	243 GPISTINPCPPCKECHKCPAPNLEGGPSVFTFPNIDKVLMSLTPKVTCTVVDVSEDDP 302	
Db	238 -----RDC-GCKPC-ICTVPEVS---SVFIPFPKPKDKVLTITLTPKVTCTVVDVSEDDP 286	
QY	303 DVQISWFVNNVEHTAQTHREDYNSTIRVSTLPIQHDQWMSGKEFKCKVNNKDLPS 362	
Db	287 EVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCKVNSAAPPAP 346	
QY	363 IERTISKIGLVRAPQVYILPPPAQLSKDKVSLTCLVGFNPGDISVEWTSNGHTENY 422	
Db	347 IERTISKIGRPAQVYITIPPKQMAKDKVSLTCLVGFNPGDISVEWTSNGHTENY 406	
QY	423 KDTAPVLDSGYSFIYKLNKMSKWEKTSFSCNVNRHEGLKNYLLKKTISRSPGK 478	
Db	407 KNTQPIMDTGSYFVYSKLVQKSNWEAGTFTCSVLHLEGLHNHHTKSLSHSPGK 462	
RESULT 14		
AAU72801		
AAU72801	standard; protein; 465 AA.	
ID	AAU72801	
XX		

249 NPCPPCKECHKCPAPNLEGGSPVFIIPPNTKIDVLMISLTTPKVTCTVVVDVSDDDVQISW 308  
 241 RDC-GCKPC-ICTVPEVS---SVFIPPKPKDLTITLTPKVTCTVVVDISKDDPEVQFSW 295  
 309 FVNNVEVHTAQTOTHTREDYNSTIRVSTLPIQHDWMSGKEFKCKVANKDLPSPIERTIS 368  
 296 FVDDVEVHTAQTOTPREQFNSTFRSVELPIHODWLNKGEKFCRVNSAAPPAPIEKTIS 355  
 369 KIKGLVRAPQVYIILPPPAEQLSRKDVSLTCLVVGFPDTSVETNSGHTTEENYKDTAPV 428  
 356 KTKGRKAPQVYITIPPPEQMAKDKVSLTCTMTDFFEDITVEQWNGQPAENYKNTQPI 415  
 429 LDSGSEFYIYSKLNMTSKWEKTDTSFSCNVRHEGLKNYLYLTKTISRSPGK 478  
 416 MNTNGSYFYYSKLVQKNSWEAGNTFTCSVLHGLHNNHTEKLSLSHSPGK 465

RESULT 15

AAR90837  
 ID AAR90837 standard; Protein; 599 AA.  
 AC AAR90837;  
 XX  
 XX  
 DT 25-JUN-1996 (first entry)  
 DE 3B1 single chain antibody from PCIB4631.  
 KW delta endotoxin; Bacillus thuringiensis; western corn rootworm;  
 KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;  
 KW antibody.  
 XX  
 OS Insecta sp.  
 XX  
 PN W09600783-A1.  
 XX  
 PD 11-JAN-1996.  
 PF 20-JUN-1995; 95WO-IB00497.  
 XX  
 PR 28-JUN-1994; 94US-0267641.  
 XX  
 PA (CIBA ) CIBA GEIGY AG.  
 XX  
 PI Carozzi NB, Koziel MG;  
 XX  
 DR WPI: 1996-077494/08.  
 DR N-PSDB; AAT15733.  
 XX  
 PT New monoclonal antibodies which bind insect gut proteins - used  
 PT partic. with toxin moieties for the control of insect pests, partic.  
 PT in plants  
 XX  
 PS Claim 8; Page 68-72; 106pp; English.

XX  
 CC AAR90829-39 are monoclonal antibodies or a binding fragments produced by  
 CC using insect guts, partic. insect brush border membranes (BBMs), esp.  
 CC corn rootworm, as antigen; immunising a donor animal with the antigen;  
 CC isolating immunocompetent B cells from the immunised animal; fusing B  
 CC cells with a tumour cell line; isolating the fused cells, culturing them  
 CC and cloning positive hybrid cells; and screening the hybrid cells for  
 CC prodn. of the required MABs. The MABs bind to the gut of a target insect  
 CC but do not bind to mammalian BBMs. The DNA sequence can be operably  
 CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,  
 CC Pseudomonas exotoxin and phytolaccin, etc.. The Abs are useful for  
 CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and  
 CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.  
 CC maize.  
 XX  
 SQ Sequence 599 AA;

Query Match 58.2%; Score 1484; DB 17; Length 599;  
 Best Local Similarity 60.0%; Pred. No. 1.5e-88;  
 Matches 282; Conservative 70; Mismatches 90; Indels 24; Gaps 8;

AAR66758;

01-SEP-1995 (first entry)

Anti-tobacco mosaic virus monoclonal Ab heavy chain.

Tobacco mosaic virus; TMV; monoclonal antibody;  
 heavy chain; virus-resistant plants; biofarming.

Synthetic.

Key Location/Qualifiers  
 Peptide 1..19  
 /label= leader  
 Peptide 20..465  
 /label= mat\_peptide  
 Domain 20..128  
 /note= "variable heavy domain"  
 Domain 129..141  
 /note= "J heavy 4 domain"  
 Domain 142..465  
 /note= "constant heavy domain"

JP06319396-A.

22-NOV-1994.

07-MAY-1993; 93JP-0131208.

07-MAY-1993; 93JP-0131208.

(NITB ) JAPAN TOBACCO INC.  
 (KURS ) KURARAY CO LTD.

WPI: 1995-040220/06.  
 N-PSDB; AAQ79930.

Transformed plant producing animal-derived anti-virus antibody -  
 esp. tobacco plants producing anti-tobacco mosaic virus  
 monoclonal antibody

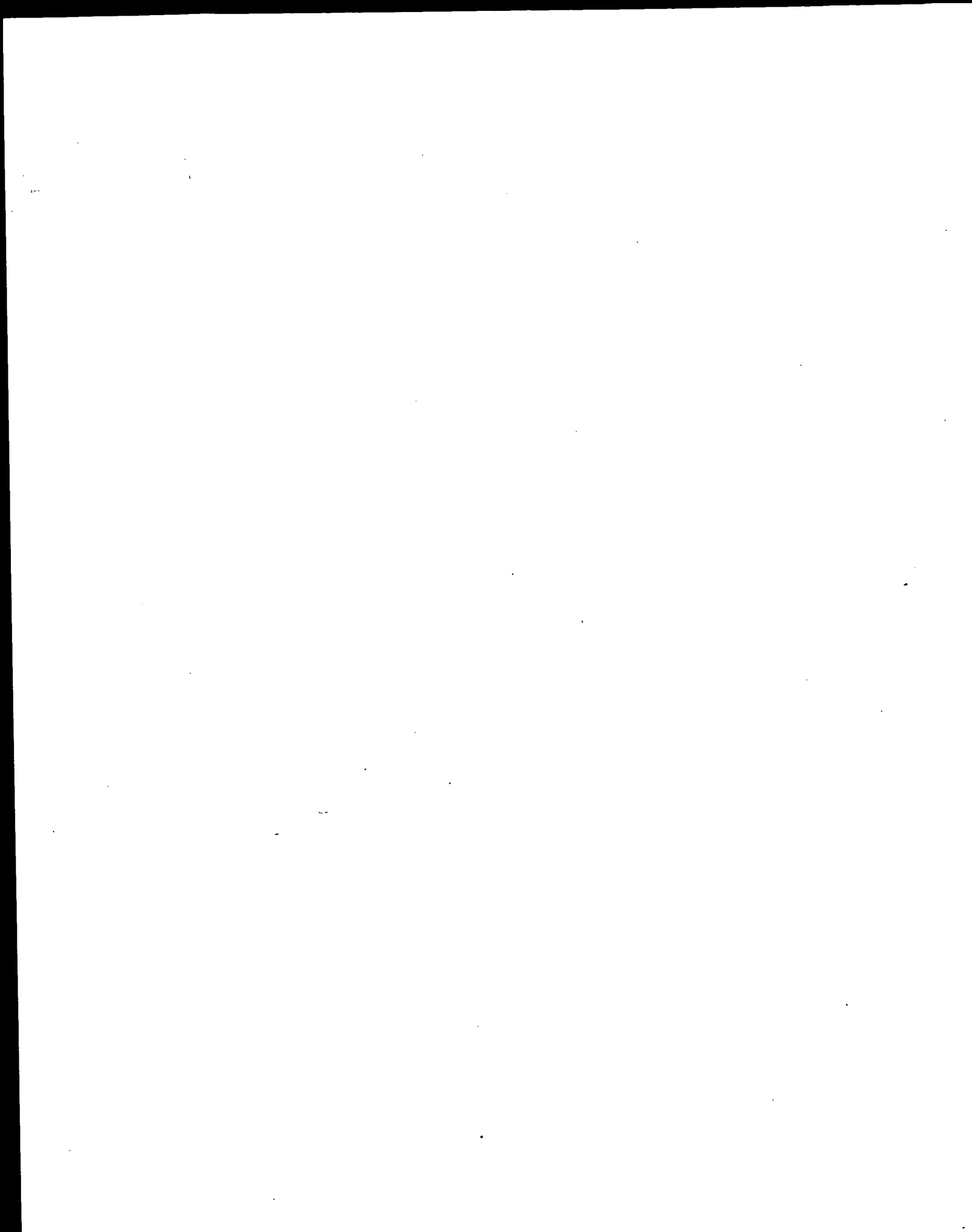
Example 2; Pages 14-15; 26pp; Japanese.

AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy  
 chains of an animal derived anti-tobacco mosaic virus (TMV)  
 monoclonal antibody. The cDNAs were incorporated into a T1  
 plasmid vector, which was incorporated into A. tumefaciens.  
 The resultant plant expression vector was used to transform  
 tobacco plants, making them TMV resistant, the plants could  
 also be biofarmed for the prodn. of anti-virus antibodies.

Sequence 465 AA;

Query Match 58.5%; Score 1493.5; DB 16; Length 465;  
 Best Local Similarity 60.0%; Pred. No. 2.8e-89;  
 Matches 282; Conservative 73; Mismatches 100; Indels 15; Gaps 6;  
 10 LVTFFSCVLSVOLQSGPLVQPSQSLTCTVSGFSLTSYGVHVRQSPGKLEWLG 69  
 10 ILSVTSYGVLSVOLQSGPLVQPSQSLTCTVSGFSLTSYGVHVRQSPGKLEW 69  
 70 IWSG-GDTDYNAFISRLSISDKNSQLFFKMNLSLRATDTAIYYCARNGDIYDFTYA 128  
 70 IYPNGDTRYTKFKGKAILTADKSSSTAYMQLSALASEDSAVVYCARGGYSWSD--YA 127  
 129 MDYWGOGTSVTVSSAKTTPPVVPLAPGCGDGTGSSVTLGCLVKGFPFVSVTWNSGSL 188  
 128 MDYWGOGTSVTVSSAKTTPPVVPLAPGAAQNTSMVTLGCLVKGFPFVSVTWNSGSL 187  
 189 SSSVHTFPALLQSLGTYMTSSVTVPSQVTCVAHPASSTVTDKLEPSGPISTI 248  
 188 SSGVHTFPVQLQSLGTYMTSSVTVPSQVTCVAHPASSTVTDKLEPSGPISTI 240

Search completed: June 18, 2003, 16:44:18  
Job time : 68.7921 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:08:07 ; Search time 1558.31 Seconds  
(without alignments)  
101/74.698 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 acaccccttgcgtgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hic.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hic.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pln.\*

21: em\_gss\_vrt.\*

22: em\_gss\_fun.\*

23: em\_gss\_mam.\*

24: em\_gss\_mus.\*

25: em\_gss\_other.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	878	89.7	939	11 AK002514	AK002514 Mus muscu
2	702.8	71.8	896	13 BG969371	BG969371 602836854
3	685.2	70.0	964	13 BG966302	BG966302 602832780
4	674.4	68.9	935	11 BC031349	BC031349 Mus muscu
5	674	68.8	805	13 B1454240	B1454240 603170666
6	672.6	68.7	857	14 BQ960162	BQ960162 AGENCOURT

7	668.2	68.3	721	13	BG967689	BG967689 602833496
8	640	65.4	871	14	BQ956722	BQ956722 AGENCOURT
9	637.2	65.1	944	12	BF687485	BF687485 602102475
10	636.8	65.0	901	14	BQ943305	BQ943305 AGENCOURT
11	628	64.1	874	12	BG518527	BG518527 602578261
12	620.8	63.4	950	12	BF162625	BF162625 601770270
13	618.6	63.2	793	13	B1105963	B1105963 602889017
14	607.6	62.1	712	13	B1100311	B1100311 602885776
15	605	61.8	705	13	BG967208	BG967208 602833891
16	594.4	60.7	967	12	BF687410	BF687410 602102583
17	593.8	60.7	830	13	B1455041	B1455041 603173343
18	592.4	60.5	974	14	BQ959869	BQ959869 AGENCOURT
19	590.4	60.3	823	12	BF580331	BF580331 602097072
20	588.6	60.1	671	13	BM194931	BM194931 L0703D04-
21	586.6	59.9	778	13	BG964076	BG964076 602828830
22	584.6	59.7	606	14	BQ922747	BQ922747 AGENCOURT
23	579	59.1	921	14	BQ924805	BQ924805 AGENCOURT
24	578.2	59.1	935	13	BG967882	BG967882 602833124
25	577.2	59.0	764	13	B1455983	B1455983 603171949
26	573.4	58.6	931	14	BQ959083	BQ959083 AGENCOURT
27	572	58.4	770	13	BG965872	BG965872 602829638
28	571	58.3	611	14	BQ175762	BQ175762 UI-M-DJ2-
29	571	58.3	781	13	B1152656	B1152656 602918350
30	570.2	58.2	594	14	BQ175706	BQ175706 UI-M-DJ2-
31	568	58.0	585	13	BM194777	BM194777 L0700H12-
32	567	57.9	886	14	BQ940987	BQ940987 AGENCOURT
33	566.6	57.9	915	14	BQ949447	BQ949447 AGENCOURT
34	566.2	57.8	785	14	BQ940341	BQ940341 AGENCOURT
35	561.8	57.4	959	14	BQ939046	BQ939046 AGENCOURT
36	558.2	57.0	607	12	BF580281	BF580281 602097014
37	556.8	56.9	569	12	BF580308	BF580308 602097044
38	554.2	56.6	643	12	BF579280	BF579280 602093454
39	547.4	55.9	553	13	BM194877	BM194877 L0702E09-
40	547.2	55.9	926	14	BQ959057	BQ959057 AGENCOURT
41	545.4	55.7	674	12	BF582339	BF582339 602101170
42	541.2	55.3	827	13	B1152061	B1152061 602916512
43	540.6	55.2	698	13	B1109045	B1109045 602896878
44	539.4	55.1	693	13	BM171763	BM171763 Imageqc.5
45	536.4	54.8	851	13	B1101548	B1101548 602887347

#### ALIGNMENTS

RESULT 1	AK002514	939 bp	mRNA	linear	HTC 19-JAN-2002
LOCUS	AK002514				
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010P20:immunoglobulin kappa chain variable 28 (V28), full insert sequence.				
ACCESSION	AK002514				
VERSION	AK002514.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:0610010P20.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE 2					
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				









This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein  
This clone has the following problem: no cloning site / microdeletion.

FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. <b>Robustness:</b> The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. <b>Interpretability:</b> The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. <b>Scalability:</b> The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. <b>Real-time Processing:</b> The model supports real-time data processing, enabling immediate insights and decision-making.	Model Performance Metrics
6. <b>Integration with Existing Systems:</b> The model seamlessly integrates with existing data management and analytics systems.	Model Performance Metrics
7. <b>Customizable Parameters:</b> The model offers customizable parameters to tailor its performance to specific use cases.	Model Performance Metrics
8. <b>Compliance with Regulations:</b> The model adheres to relevant data protection and privacy regulations, ensuring ethical data usage.	Model Performance Metrics
9. <b>Extensive Documentation:</b> Comprehensive documentation is provided, detailing the model's architecture, training process, and usage instructions.	Model Performance Metrics
10. <b>Active Support:</b> Users receive active support and assistance from the development team to address any issues or queries.	Model Performance Metrics

```

Location/Qualifiers
1. 935
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:J514385"
/tissue_type="Mammary gland, lactating mouse"
/clone_lib="Soares_mammary_gland_NLMG"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac"
251 a 247 c 208 g 229 t

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BASE COUNT  
ORIGIN

251 a 247 c 208 g 229 t

h 58.9%; Score 674.4; DB 11; Length 935;  
 Similarity 84.3%; Pred. No. 9.8e-95;  
 89; Conservative 0; Mismatches 131; Indels 16; Gaps 2;

7 CTCAGGTCCTGGCGTTGCTGCTGCTGGCTTACAGGTGCCAGATGTGACATCCAGATGA 116  
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 1 CTGAGTTCTGCGGCGTGTGTGCTCTGGATCCCTGGAGCCCATTTGGGGATATTGTGATGA 60  
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 7 CTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCCACATCACATGTCGAG 176  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 CTCAGGCTGCACCTCTGTACCTCTGCATCTCTGGAGAGTCAGTATCCATCTCCTCGAGGT 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 7 CAAGTGGGAATATTC-----AAAATTATTAGCATGGTATCAGCAGACAC 221  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 CTAGTAAAGTCTCCTGCATATTGATGCCAACACTTATTATTGGTTCTCGCAGGC 180  
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 2 AGGMAAATCTCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCAT 281  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 CAGGCCAGTCTCTCAGCTCCTGTATATCGGATGTCCAACCTTGCTCAGGAGTCCCAG 240  
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 2 CAAGGTTCACTGGCAGTGGATCAGGAACACAATATCTCTCAAGATCAACAGCCTGCAGC 341  
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 1 ACAGGTTCACTGGCAGTGGGTGAGAACTGCTTCACACTGGAATCAGTAGAGTGGAG 300  
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 2 CTGAAGATTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACAGTTCGGAG 401  
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 1 CTGAGGATGTGGGTGTTTATTACTGTATGCAACATCTAGATATCCGTACAGTTCGGAG 360  
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 2 GGGGGACCAAGCTGGAATATAAACGGGCTGATGTGCACCAACTGTATCCATCTTCCCCAC 461  
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 1 GGGGGACCAAGCTGGAATATAAACGGGCTGATGTGCACCAACTGTATCCATCTTCCCCAC 420  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2 CATCCAGTGAGCAGTTAAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAATCTCT 521  
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 1 CATCCAGTGAGCAGTTAAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAATCTCT 480  
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 1 ACCCCAAAGACATCAATGTCAAGTGGGAAGATTGATGGCAGTGAACGACAAATGGCGTCC 540  
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 1 TGAACAGTTGGACTGATCAGGACAGCAAGACAGCACTACAGCATGAGCAGCACCCCTCA 641  
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 1 TGAACAGTTGGACTGATCAGGACAGCAAGACAGCACTACAGCATGAGCAGCACCCCTCA 600  
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 1 GAGCGCCACCAACAGCTCCCGAGCTCCATCTTCTTCCCTTAAGGCTTTGGAGGCT 821  
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[illegible]

RESULT 5  
BI454240

LOCUS	BI454240	805 bp	mRNA	linear	EST 21-AUG-2001
DEFINITION	603170666F1 NCI_CGAP_Mam5 musculus cDNA clone IMAGE:5250017 5',				
ACCESSION	BI454240				
VERSION	BI454240.1				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 805)				
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11631 row: d column: 18 High quality sequence stop: 790.				

FEATURES  
source

FEATURES	source
align quality sequence stop: 790.	
Location/Qualifiers	
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/strain="C57BL/6J"	
/db_xref="taxon:10090"	
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/lab_host="DH10B"	
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"	
230 a	209 c 186 g 180 t
BASE COUNT	

BASE COUNT	NIH*	
ORIGIN	230 a	209 c
180 t	186 g	

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	Best Local Similarity	94.0%;	Pred. No. 1.2e-94;		
	Matches 756;	Conservative	0; Mismatches	40; Indels	8; Gaps
Y	30	GATCACACACATCATGATGTGCTACTCAGGTCTCTGGCGTCTGCTGCTGC - TGTGGCTT	88		
b					
	1	GAAGAACACACACATGATGTGCCACTCAGGTCTCTGGGTTGCTGCTGCTTGGCTT	60		
Y	89	ACAGTGGCCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTG	148		
b					
	61	ACAGAGGCCAGATGTGACATCCAGATCACTCAGTCTCCAGCCTCCCTCTCTGCATCTGTG	120		
Y	149	GGAGAAACTGTCCACCATCACATGTGCAGCAAGTGGGAAATATTTCAAATATTTTAGCATGG	208		
b					
	121	GGAGAACTGTCCACCATCACATGTGCAGCAAGTGGGAAATATTTCAAATATTTTAGCATGG	180		

209	TATCAGCAGACACACAGGAAAATCTCTCAGCTCTCTGGTCTATTCTGCAGAAACCTTAGCA	268
181	TATCAGCAGAAACACAGGAAAATCTCTCAGTCTCTGGTCTATAATGCAGAAACCTTAGCG	240
269	GATGCTGTGCCATCAAGCTTCAGTGGCAGTGSATCAGAACACAAATATCTCTCAAGATC	328
241	GAAGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGCACACAGTTTTCTTAAGATC	300
329	AACAGCCTGCAGCCTGAAGATTTTGGGAGTTTATTACTGTCAACATTTTTTGGAGTACTCCG	388
301	RACAGCCTGCAGCCTGAAGATTTTGGGACTTATTACTGTCAACATCATAAAGGCACTCCG	360
389	TACAGCTTCGGAGGGGGACCAAGCTGGAAATAAAGCGGCTGATGCTGCACCAACTGTA	448
361	TACAGCTTCGGAGGGGGACCAAGCTGGAAATAAAGCGGCTGATGCTGCACCAACTGTA	420
449	TCCATCTTCCCACCATTCCAGTGAGCAGTTAAACATCTGGAGGTGCTCAGTCTGCTGCTC	508
421	TCCATCTTCCCACCATTCCAGTGAGCAGTTAAACATCTGGAGGTGCTCAGTCTGCTGCTC	480
509	TTTGAAC - AACTTCTTACCCCAAGACATCAATGTCAAGTGGGAAGATTGATGGCATGTGAACG	567
481	TTTGAACAACTTCTACCCCAAGACATCAATGTCAAGTGGGAAGATTGATGGCAGTGAACG	540
568	ACAAATGGCGTCTGAACAGTTTGACGTGATCAGCAGACAGCAAGACAGCACCTACAGCAT	627
541	ACAAATGGCGTCTGAACAGTTTGACGTGATCAGCAGACAGCAAGACAGCACCTACAGCAT	600
628	GAGCAGACCCCTCAGTTTGACCAAGGAGCAGTATGAACGACATACACAGCTATACCTGTGA	687
601	GAGCAGACCCCTCAGTTTGACCAAGGAGCAGTATGAACGACATACACAGCTATACCTGTGA	660
688	GG - CCATTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT	746
661	GGCCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT	720
747	AGAGACAAAGTTCCTGAGA - CGCCACCAACAGCTCCCGCAGCTCCATCC - - TATCTTCC	801
721	AGAGACAAAGTTCCTGAGAAGCCACCAACCCAGCTCCCGCAGCTCCATCTTCTTTCC	780
802	CTTCTAAGGTCTTGGAGGCTTCCC	825
781	CTTCTAAGGTCTTGGAGGCTTCCC	804

RESULT 6  
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 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 857)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
 Tissue procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14022 row: c column: 20  
 High quality sequence stop: 632.

[illegible]



[illegible]







277 GCATCAAGGTTTCTAGTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 336  
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241 GCCATCAGGTTTCTAGTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 300  
|||||  
337 GCAGCCTGAAGATTTTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 396  
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301 GCAGCCTGAAGATTTTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 359  
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397 CGGAGGGGGGACCAAGCTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 456  
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360 CGGAGGGGGGACCAAGCTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 419  
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420 CCCACCATCCAGTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 479  
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540 CGTCTGAAGCTGGAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCT 598  
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RESULT 13  
BI105963  
NCI\_CGAP\_Lu29

793 bp mRNA linear EST 26-JUN-2001  
musculus cDNA clone IMAGE:5036044 5',  
mRNA sequence.

BI105963  
NCI\_CGAP\_Lu29

793 bp mRNA linear EST 26-JUN-2001  
musculus cDNA clone IMAGE:5036044 5',  
mRNA sequence.

BI105963.1 GI:14556856  
EST.  
house mouse.  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 793)

NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1100 row: a column: 05

High quality sequence stop: 769.  
Location/Qualifiers  
1..793

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5036044"

/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"

/note="Organ: lung; Vector: pCMV-Sport6; Site:1: SalI;  
Site:2: NotI; Cloned unidirectionally. Primer: oligo dt.  
Library constructed by Life Technologies. Investigator

BASE COUNT 212 a 230 c 166 g 185 t  
ORIGIN  
Query Match 63.2%; Score 618.6; DB 13; Length 793;  
Best Local Similarity 87.8%; Pred. No. 4e-86;  
Matches 686; Conservative 0; Mismatches 94; Indels 1; Gaps 1;  
QY 188 ATCAAAATTTATTTAGTGGTATCAGCAGACAGAGGAAATCTCTCAGTCTCTGGTC 247  
Db 10 AGTGAAATTTTATCAGTGGTATCAGCAGACAGAGGAAATCTCTCAGTCTCTGGTC 69  
QY 248 TATCTGCAAAACCTTAGCAGATGTTGCCATCAAGTTTCAGTGGCAGTGGATCAGGA 307  
Db 70 TATCCTACATCGGACCTGGCTTCTGGAGTCCCTGCTCTCAGTGGCAGTGGGACTGG 129  
QY 308 ACACAATATTTCTCAAGATCAACAGCCTGAGCCTGAAGATTTTGGAGTGTATTACTGT 367  
Db 130 ACCTTACTCTCTCAATCAGCAGCATGAGGCTGAAGATGCTGCCACTTATTTCTTGC 189  
QY 368 CAACATTTTGGAGTACTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAACGG 427  
Db 190 CAGCAGTATCATAGTTACCCACGGACGTTCCGTGGAGCACCAGCTGGAATCAACGG 249  
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Db 250 GCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGGAGCTTAACTCTGGA 309  
QY 488 GGTGCTCAGTCGTTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGG 547  
Db 310 GGTGCTCAGTCGTTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGG 369  
QY 548 AAGATTGATGSCAGTGAACGACAAATGGCTCTCTGAACAGTTGGACTGATCAGCAGACG 607  
Db 370 AAGATTGATGSCAGTGAACGACAAATGGCTCTCTGAACAGTTGGACTGATCAGCAGACG 429  
QY 608 AAGACAGCCTTACAGCATGAGCAGCACCTTACCTGACCAAGGACGAGTATGAACGA 667  
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QY 668 CATACAGCTATACCTGTGAGGCGCCTCAACAGACATCAACTTCCACCATTTGCAAGACG 727  
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QY 728 TTCAACAGGAATGAGTGTAGAGACAAAGTCTTGAGACGAGGCTTCCACCAAGGACGCTCC 787  
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QY 908 CATGCTTAATTTGCAAGAAATATTCAA-TAAAGTGAAGTCTTTGCAAAAAAATAAAAA 966  
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QY 967 A 967  
Db 790 A 790

RESULT 14  
BI100311  
NCI\_CGAP\_Kid14

712 bp mRNA linear EST 26-JUN-2001  
musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311  
NCI\_CGAP\_Kid14

712 bp mRNA linear EST 26-JUN-2001  
musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311  
NCI\_CGAP\_Kid14

712 bp mRNA linear EST 26-JUN-2001  
musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311.1 GI:14551204  
EST.

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

BI100311  
602885776F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311  
602885776F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311.1 GI:14551204  
EST.

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

BI100311  
602885776F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311  
602885776F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5041194  
5', mRNA sequence.

BI100311.1 GI:14551204  
EST.

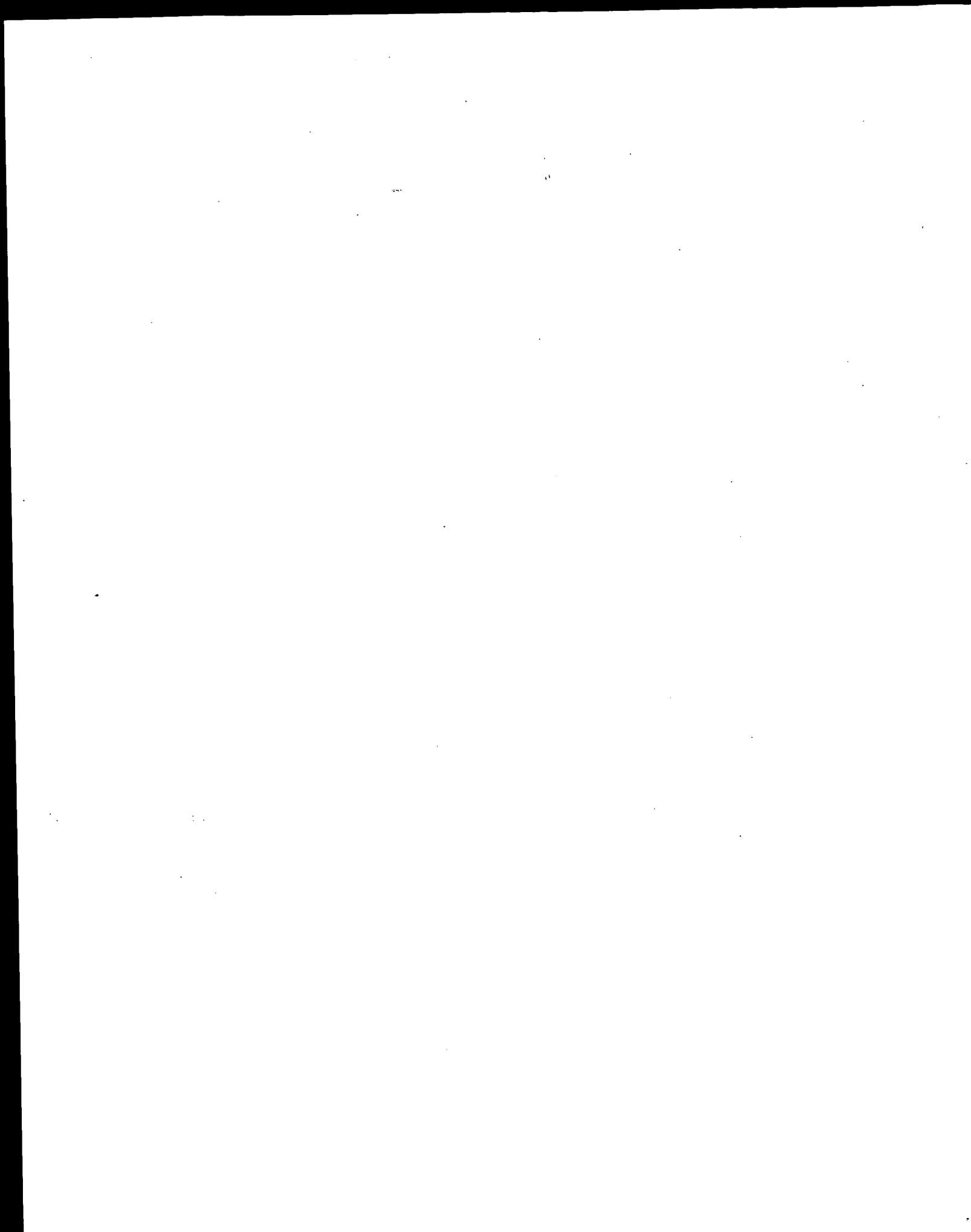


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579 TCTGAACAGTTGGACTGATCAGGACAGCAAGACAGCAGCCTACAGCATGAGCAGCACCC 538
301 TCTGAACAGTTGGACTGATCAGGACAGCAAGACAGCAGCCTACAGCATGAGCAGCACCC 360
639 TCACGTTGACCAAGGACGAGTATGAACGACATACAGCTATACCTGTGAGGCCACTCACA 698
361 TCACGTTGACCAAGGACGAGTATGAACGACATACAGCTATACCTGTGAGGCCACTCACA 420
699 AGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGGT 758
421 AGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGGT 480
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481 CCTGAGCGCCACCAAGGACCTCCCGAGCTCCATCTCTTCCCTTCTAAGGTCTTGGAG 540
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541 GCTTCCCAAGGACCTACACTGTTGGGCTGCTCCAAACCTCCTCCCGACCTCCTTC 600
879 TCCTCTCCCTCCCTTCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAATAA 938
601 TCCTCTCCCTCCCTTCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAATAA 660
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Search completed: June 24, 2003, 01:20:04  
 Job time : 1567.31 secs









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478 AACATCTGGAGGTCCTCAGTCGCTGCTTCTTGAACAACATTTACCCCAAGACATCAA 537  
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1724 AACATCTGGAGGTCCTCAGTCGCTGCTTCTTGAACAACATTTACCCCAAGACATCAA 1783  
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538 TGTCAGTGGAGATGATGATGCGAGTGAACGACAAATGGCGTCTGACAGTTGGACTGA 597  
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1784 TGTCAGTGGAGATGATGATGCGAGTGAACGACAAATGGCGTCTGACAGTTGGACTGA 1843  
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598 TCAGGACAGCAAGACAGCAGCTACAGCATGAGCAGCAGCCTCAGCTTGACCAAGGACGA 657  
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1844 TCAGGACAGCAAGACAGCAGCTACAGCATGAGCAGCAGCCTCAGCTTGACCAAGGACGA 1903  
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658 GTATGAAGGACATTAACAGTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCAT 717  
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1904 GTATGAAGGACATTAACAGTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCAT 1963  
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718 TGTCAGAGGCTTCAACAGGAATGAGTGTAGAGACAAAGGTCCTGAGAGCCACACACAG 777  
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1964 TGTCAGAGGCTTCAACAGGAATGAGTGTAGAGACAAAGGTCCTGAGAGCCACACACAG 2023  
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2084 ACCACTGTGGGGTCTCCAAACCTCTCCACCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2143  
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## RESULT 5

S-10-219-051B-12710  
Sequence 12710, Application US/10219051B  
GENERAL INFORMATION:  
APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
APPLICANT: Hospital / Bayer AG  
TITLE OF INVENTION: Nucleotide sequences involved in pain  
FILE REFERENCE: Lea 35693 Foreign Countries  
CURRENT APPLICATION NUMBER: US/10/219,051B  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 60/312,147  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/346,382  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 60/333,347  
PRIOR FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 14715  
SOFTWARE: Perl script  
SEQ ID NO 12710  
LENGTH: 959  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: EMBL / L22655  
DATABASE ENTRY DATE: 2000-03-04  
S-10-219-051B-12710

Query Match 53.6%; Score 524.6; DB 10; Length 959;  
Best Local Similarity 75.3%; Pred. No. 5e-90;  
Matches 716; Conservative 0; Mismatches 209; Indels 26; Gaps 4;

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QY 104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGAGAAACACTGTACC 163  
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Db 78 GATGTTGTGATGACCCAGACTCCAGTGTCTTGTGTCAGTTGCCATTGGACACACAGCTCC 137  
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QY 164 ATCATATGTCGAGCAAGTGGG-----AATATCAAATATTTAGCATGG 208  
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## RESULT 6

US-10-236-051-7  
; Sequence 7, Application US/10236051  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: LETURCO, Didier J.  
; APPLICANT: MORIARTY, Ann M.  
; APPLICANT: ULEVITCH, Richard J.



```

; APPLICANT: TOBIAS, Peter S.
; APPLICANT: MATHISON, John C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRI1140-4
; CURRENT APPLICATION NUMBER: US/10/236,051
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/170,769
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/373,297
; PRIOR FILING DATE: 1995-01-23
; PRIOR APPLICATION NUMBER: PCT/US94/05898
; PRIOR FILING DATE: 1994-05-27
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(633)
; OTHER INFORMATION: CDR1=Nucleic acids 61-93; CDR2=Nucleic acids 139-159;
; OTHER INFORMATION: CDR3=Nucleic acids 256-28
; PS-10-236-051-7

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[illegible]

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Db      601  CCATTGTCAAGAGCTTCAACAGGAATGATGTG  633C
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        US-10-424-599-65669
        ; Sequence 65669, Application US/10424599
        ; GENERAL INFORMATION:
        ; APPLICANT: La Rosa Thomas J
        ; APPLICANT: Kovalic David K
        ; APPLICANT: Zhou Yihua
        ; APPLICANT: Cao Yongwei
        ; TITLE OF INVENTION: Soy Nucleic Acid Molecules a
        ; TITLE OF INVENTION: Plants and Uses Thereof for
        ; FILE REFERENCE: 38-21(53223)B
        ; CURRENT APPLICATION NUMBER: US/10/424,599
        ; CURRENT FILING DATE: 2003-04-28
        ; NUMBER OF SEQ ID NOS: 285684
        ; SEQ ID NO 65669
        ; LENGTH: 870
        ; TYPE: DNA
        ; ORGANISM: Glycine max
        ; FEATURE:
        ; - OTHER INFORMATION: Clone ID: PAT_MRT3847_30314C
        ; US-10-424-599-65669

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Query Match	48.28;	Score	471.4;	DB	10;	Length	870;
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Gaps							
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	162	CCATCACATGTCGAGCAAGTGGGAATATTCAA-----AATTATTATG	203				
	67	CTATGAGCTGCAAGTCAGTCAAGTCTTTTATGGATTTGGAATCAAGAGAGCTGTTATG	126				
	204	CATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCT	263				
	127	TCTGGCACCAAGAAACACAGGCAGACTCTTAACCACTGATCACTGGGCATCCAATA	186				
	264	TAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCATGTGATCAGAAACAAATATTTCTCTCA	323				
	187	GGGAACCTGGGGTCCCTGATGCTGTTTATAGGCAGTGGATCTGACACAGATTTTACTCTCA	246				
	324	AGATCAACAGCCTGCAGCCTGGAAGATTTTGGGAGTTTATTACTGTCAACATTTTTGGAGTA	383				
	247	CCATTAGCAATATGCAAGGCTGAAGATGTGGGTTTTTATTACTGTGACGACGATTTAGACA	306				
	384	CTCCGTACAGTTTCGGAGGGGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAA	443				
	307	TTCCCT-CAGGTTTCGGTTCGGGACCAAGCTGGAGATCAACGGGCTGATGCTGCACCAA	365				
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	366	CTGTATCTATCTTCCGCCCATCCACGGAACAGTTAGCAACTGGAGGTGCTCAGTCGTGT	425				
	504	GCCTTCTGAAACAATTTCTACCCCAAGACATCAATGTCAAGTGGAGATTTGATGGCACTG	563				
	426	GCCTCATGAACACTTCTATCCCAAGACATCAGTGTCAAGTGGGAAGATTTATGGCACTG	485				
	564	AACGACAAAATGGCGTCCCTGAACAGTTGGACTGTATCAGGACAGAAAGACAGCACTACA	623				
	486	AACGACGAGATGTTGTCCTGGACAGTGTACTGTATCAGGACAGAAAGACAGCACTACA	545				
	624	GCATGACGACCCCTCAGTTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCT	683				
	546	GCATGACGACCCCTCTCTGTTGACCAAGGCTGACTATGAAGTCTATAACCTCTATACCT	605				
	684	GTGAGGCCACTCACAGACATCACTTCAACCATTTGTCAAGAGCTTCAACAGGAATGAGT	743				
	606	GTGAGGTTTCTATAGACATCATCTCTCACCGCTGGTCAAGAGTTCACAGGAATGAGT	665				



Db 97 TCCACATCAGTAGGAGACAGGTCAGCATCACCTGCAAGGCCAGTCAGGATGGGTACT 156  
QY 197 TATTTAGCATGTATCAGACAGACAGGAAATCTCTCAGCTCCTGTCTATTTCTGCA 256  
Db 157 GCTGTAGCCTGTGTATCAACAGAAACAGGCAATCTCTTAACTACTGATTTACTGGCA 216  
QY 257 AAAACCTTAGCAGATGGTGTCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACAATAT 316  
Db 217 TCCACCCGGCAGCTGGAGTCCCTGATCGCTTCACAGGCAAGTGGATCTGGACAGATTTC 276  
QY 317 TCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGAGATTATCTGCTCAAACTTTT 376  
Db 277 ACTCTCACCATTAGCAATGTGCAGTCTGAAGCTTGGCAGATTTATTTCTGTCAGCAATAT 336  
QY 377 TGGAGTACTCCGTACACGTTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT 436  
Db 337 AGCAGCTATCGG---ACGTTCCGTTGGAGCCACCAAGCTGGAAATCAACGGGCTGATGCT 393  
QY 437 GCACCAACTGTATCCATCTCCACCATCCAGTGCAGTGAAGTTAAACATCTGGAGTCCCTCA 496  
Db 394 GCACCAACTGTATCCATCTCCACCATCCAGTGCAGTGAAGTTAAACATCTGGAGTCCCTCA 453  
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QY 557 GGCAGTGAACGACAAAATGGGCTCTGTAACAGTTGGAGTGAAGTTAAACATCTGGAGTCCCTCA 616  
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QY 617 ACCTACAGCATGAGCAGCAGCCTCAGCTTGACCAAGGAGCAGTATGAACGACATAACAGC 676  
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QY 737 AATGAGTGTTA 747  
Db 694 AATGAGTGTTA 704

## RESULT 10

S-10-286-132A-22

Sequence 22, Application US/10286132A

## GENERAL INFORMATION:

APPLICANT: Zhou, Tong  
APPLICANT: Kimberly, Robert P.  
APPLICANT: Koopman, William J.  
APPLICANT: LoBuglio, Albert S.  
APPLICANT: Buchsbaum, Donald J.

TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED

FILE REFERENCE: 21085.002907

CURRENT APPLICATION NUMBER: US/10/286,132A

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/346,402

PRIOR FILING DATE: 2001-11-01

PRIOR APPLICATION NUMBER: PCT/US01/14151

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/201,344

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 705

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct

S-10-286-132A-22

## Query Match

Best Local Similarity 47.1%; Score 461.4; DB 9; Length 705;

Matches 547; Conservative 81.5%; Pred. No. 4.7e-78;

Mismatches 121; Indels 3; Gaps 1;

QY 77 CTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCAGTCTCAGGCTCCCTA 136

Db 37 CTGTTTCTGTTTGCAGGTGTGAAGGAGACATTTGTGATGACCCAGTCTCACAATTCATG 96

QY 137 TCTGCATCTGTGGGAAACTGTCAACATCAGATGTCGAGCAAGTGGGAATATTTCAAAAT 196

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Db 277 ACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATTTATTTCTGTCAGCAATAT 336

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QY 437 GCACCAACTGTATCCATCTCCACCATCCAGTGCAGTGAAGTTAAACATCTGGAGTCCCTCA 496

Db 394 GCACCAACTGTATCCATCTCCACCATCCAGTGCAGTGAAGTTAAACATCTGGAGTCCCTCA 453

QY 497 GTCGTGTCTTCTTGAACAACCTTCTGAAACAGTTGGAGTGAAGTTAAACATCTGGAGTCCCTCA 556

Db 454 GTCGTGTCTTCTTGAACAACCTTCTGAAACAGTTGGAGTGAAGTTAAACATCTGGAGTCCCTCA 513

QY 557 GGCAGTGAACGACAAAATGGGCTCTGTAACAGTTGGAGTGAAGTTAAACATCTGGAGTCCCTCA 616

Db 514 GGCAGTGAACGACAAAATGGGCTCTGTAACAGTTGGAGTGAAGTTAAACATCTGGAGTCCCTCA 573

QY 617 ACCTACAGCATGAGCAGCAGCCTCAGCTTGACCAAGGAGCAGTATGAACGACATAACAGC 676

Db 574 ACCTACAGCATGAGCAGCAGCCTCAGCTTGACCAAGGAGCAGTATGAACGACATAACAGC 633

QY 677 TATACCTGTGAGGCCACTCACAAGACATCACTTCAACCATTTGTCAAGAGCTTCAACAGG 736

Db 634 TATACCTGTGAGGCCACTCACAAGACATCACTTCAACCATTTGTCAAGAGCTTCAACAGG 693

QY 737 AATGAGTGTTA 747

Db 694 AATGAGTGTTA 704

## RESULT 11

US-10-281-479A-22

Sequence 22, Application US/10281479A

## GENERAL INFORMATION:

APPLICANT: The UAB Research Foundation  
APPLICANT: Zhou, Tong

APPLICANT: Ichikawa, Kimihisa

APPLICANT: Kimberly, Robert P.

APPLICANT: Koopman, William J.

APPLICANT: Oshumi, Jun

APPLICANT: LoBuglio, Albert S.

APPLICANT: Buchsbaum, Donald J.

TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS

TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T

FILE REFERENCE: 21085.002906

CURRENT APPLICATION NUMBER: US/10/281,479A

CURRENT FILING DATE: 2003-01-28

PRIOR APPLICATION NUMBER: 60/391,478



RESULT 13  
US-09-726-219A-189  
; Sequence 189, Application US/09726219A  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Medical Research Council  
; APPLICANT: McCafferty, John  
; APPLICANT: Pope, Anthony  
; APPLICANT: Johnson, Kevin  
; APPLICANT: Hoogenboom, Hendricus  
; APPLICANT: Griffiths, Andrew  
; APPLICANT: Jackson, Ronald  
; APPLICANT: Holliger, Kasper  
; APPLICANT: Marks, James  
; APPLICANT: Clarkson, Timothy  
; APPLICANT: Chiswell, David  
; APPLICANT: Winter, Gregory  
; APPLICANT: Bonert, Timothy  
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
; FILE REFERENCE: 213839-00013  
; CURRENT APPLICATION NUMBER: US/09/726,219A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB 9015198.6  
; PRIOR FILING DATE: 1990-07-10  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9024503.6  
; PRIOR FILING DATE: 1990-11-12  
; PRIOR APPLICATION NUMBER: GB 9104744.9  
; PRIOR FILING DATE: 1991-03-06  
; PRIOR APPLICATION NUMBER: GB 9110549.4  
; PRIOR FILING DATE: 1991-05-15  
; PRIOR APPLICATION NUMBER: PCT/GB91/01134  
; PRIOR FILING DATE: 1991-07-10  
; PRIOR APPLICATION NUMBER: US 07/971,857  
; PRIOR FILING DATE: 1993-01-08  
; PRIOR APPLICATION NUMBER: US 08/484,893  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 272  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 189  
; LENGTH: 1526  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: nucleotide sequence of Fab D1.3 from genetically engineered anti-  
; OTHER INFORMATION: hen egg-white lysozyme (HEW) monoclonal antibody

[illegible]

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Db	1113	GAAGATTTTGGAGTTATTACTGTCAACATTTTGGAGTACTCTCGACGTTCCGGTGA	1172
QY	404	GGGACCAAGCTGGAAATAAAACGGCGTGTGCTGCACCAACTGTATCCATCTTCCCACCA	463
Db	1173	GGCACCAAGCTCGAGATCAAAACGGAGTGTGGCTGCACCATGTGCTTCATCTTCCCGCCA	1232
QY	464	TCCAGTGAGCAGTTAAACATCTGGAGGTGCCTCAGTCGTGCTTCTTTGAACAACCTTCAC	523
Db	1233	TCTGATGAGCAGTTGAAATCTGGAACGTGCCTCTGTTGTGTGCTCTGATCACTTCTAT	1292
QY	524	CCCAAAACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAAATGGCTGCTG	583
Db	1293	CCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAAATCGGGTAACTCCAG	1352
QY	584	AACAGTTGGACTGATCAGGACAGCAAGACAGCACTTACAGCATGAGCAGCACTCCACG	643
Db	1353	GAGAGTGTCAAGACAGGACAGCAGGACAGCAGCACTTACAGCCTCAGCAGCACTTCAGC	1412
QY	644	TTGACCAAGACAGGATATGAACGACATAACAGCTATACCTGTGAGGCGCACTCAACAACA	703
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QY	704	TCAACTTCAACCCATTGTCAAGAGCTTCAACAGCAAGTGAAGTTAGAGACAA	754
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RESULT 14  
US-10-384-933-10  
; Sequence 10, Application US/10384933  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, Nobufusa  
; APPLICANT: Haruyama, Hideyuki  
; APPLICANT: Nakahara, Kaori  
; APPLICANT: Tamaki, Ikuro  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Pas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT APPLICATION NUMBER: US/10/384,933  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 165

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/ SEQ ID NO: 714
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/ LOCATION: (1)..(714)
/ FEATURE:
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/ NAME/KEY: mat peptide
/ LOCATION: (61)..(714)
/ FEATURE:
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/ NAME/KEY: sig peptide
/ LOCATION: (1)..(60)
/ US-384-933-10

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Query Match 45.6%; Score 446.6; DB 10; Length 714;  
Best Local Similarity 79.0%; Pred. No. 3e-75;  
Matches 549; Conservative 0.0; Miscellaneous 124

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 Qy 123 CTCAGGCTCCCTATCTGCATCTGTGGGAAACTGTCCACCATCACATGTCGAGCAAGTG 182  
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183 GGAATATTCAAA-----TTATTAGCATGTGTATCAGCAGACAGGGAAT 230  
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591 GGACTGATCAGGACAGCAAGACAGCAGCTTACAGATGAGCAGACCCCTCAGTTGACCA 650  
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RESULT 15

S-10-251-215-47

Sequence 47, Application US/10251215

GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.

APPLICANT: Kretz-Rommel, Anke

APPLICANT: Frederickson, Shana

TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED

TITLE OF INVENTION: ANTI-PDGF ANTIBODIES

FILE REFERENCE: 1087-36

CURRENT APPLICATION NUMBER: US/10/251,215

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: US 60/323,537

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/323,544

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/379,980

PRIOR FILING DATE: 2002-05-13

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patent version 3.2

SEQ ID NO 47

LENGTH: 702

TYPE: DNA

ORGANISM: murine

S-10-251-215-47

Query Match

Best Local Similarity

Matches 522; Conservative

45.5%; Score 445.2; DB 8; Length 702;

82.1%; Pred. No. 5.4e-75;

2; Mismatches 110; Indels 2; Gaps 1;

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QY 172 TCGAGCAAGTGGGAATATTCAAAATATTATTAGCATGGTATATCAGCAGACACAGGAAATC 231  
Db 75 C--AACTGCCAGCTCAAGTGTAAAGTACATGCCACTGGTTCAGCAGAAAGCCAGGCATTC 132  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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5	693.4	70.8	1041	3	US-07-904-074A-1
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DB	1	ACACCCCTTTGCTGGAGTCAAAATCACACTGATCACAACACAGTCATGATGCTGCCTCACTCA	60		
QY	61	GGTCTCGCGGTGCTGCTGCTGCTGGCTTACAGTGCCAGATGTCACATCCAGATGACTCA	120		
DB	61	GGTCTCGCGGTGCTGCTGCTGCTGGCTTACAGTGCCAGATGTCACATCCAGATGACTCA	120		
QY	121	GTCTCCAGCCCTCCCTATCTGTCATCTGTGGAGAAAATGTCACCATCACATGTCGAGCAAG	180		
DB	121	GTCTCCAGCCCTCCCTATCTGTCATCTGTGGAGAAAATGTCACCATCACATGTCGAGCAAG	180		
QY	181	TGGGAATATTCAAATAATTATTAGCATGGTATCAGCAGACACAGGAAAAATCTCTCGACT	240		
DB	181	TGGGAATATTCAAATAATTATTAGCATGGTATCAGCAGACACAGGAAAAATCTCTCGACT	240		
QY	241	CCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGCCATCAAGGTTAGTGGCAGTGG	300		
DB	241	CCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGCCATCAAGGTTAGTGGCAGTGG	300		
QY	301	ATCAGGAACACAATAATTCTCTCAGATCAACAGCCTGCAGCTGAAGATTTTGGGAGTTA	360		
DB	301	ATCAGGAACACAATAATTCTCTCAGATCAACAGCCTGCAGCTGAAGATTTTGGGAGTTA	360		
QY	361	TTACTGTCAACATTTTTCGGAGTACTCCGTACACGPTTCGGAGGGGGACCAAGCTGGAAT	420		
DB	361	TTACTGTCAACATTTTTCGGAGTACTCCGTACACGPTTCGGAGGGGGACCAAGCTGGAAT	420		
QY	421	AAAAGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGGACGATTAA	480		
DB	421	AAAAGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGGACGATTAA	480		
QY	481	ATCTGGAGGTGCCCTCAGTCGTGTGCTTCTTGAAACAATTTCTACCCAAGAAGCATCAAT	540		
DB	481	ATCTGGAGGTGCCCTCAGTCGTGTGCTTCTTGAAACAATTTCTACCCAAGAAGCATCAAT	540		
QY	541	CAAGTGGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCCTGAACAGTTGACATGAT	600		
DB	541	CAAGTGGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCCTGAACAGTTGACATGAT	600		
QY	601	GGACAGCAAGACAGCACCTACAGCATGAGCAGCACCCCTCAGCTTGACCAAGACAGTA	660		
DB	601	GGACAGCAAGACAGCACCTACAGCATGAGCAGCACCCCTCAGCTTGACCAAGACAGTA	660		
QY	661	TGAAGCGACATAACAGCTATACCTGTGAGGCCACTCACAAAGACATCAACTTCACCCATT	720		
DB	661	TGAAGCGACATAACAGCTATACCTGTGAGGCCACTCACAAAGACATCAACTTCACCCATT	720		
QY	721	CAAGAGCTTCAACAGGAATGAGTGTGTAGAGACAAAGGTCTGAGAGCGCCACACAGCTC	780		
DB	721	CAAGAGCTTCAACAGGAATGAGTGTGTAGAGACAAAGGTCTGAGAGCGCCACACAGCTC	780		
QY	781	CCAGCTCCATCCTATCTTCCCTTTCTAAGGCTTTGGAGGCTTCCCCACAAAGCGACCTAC	840		
DB	781	CCAGCTCCATCCTATCTTCCCTTTCTAAGGCTTTGGAGGCTTCCCCACAAAGCGACCTAC	840		
QY	841	ACTGTGGGGTGGCTCCAAACCTCTCTCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	900		

## SULT 1

GENERAL INFORMATION:  
 APPLICANT: Frank, Dara W.  
 APPLICANT: Wiener-Kronish, Jeannine  
 APPLICANT: Yahr, Timothy L.  
 APPLICANT: Sawa, Teiji  
 APPLICANT: Fritz, Robert B.  
 TITLE OF INVENTION: Method of and compositions for immunization with the  
 FILE REFERENCE: 650053.91487  
 CURRENT APPLICATION NUMBER: US/09/770,916  
 CURRENT FILING DATE: 2001-01-26  
 PRIOR APPLICATION NUMBER: 09/448,339  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: 60/109,952  
 PRIOR FILING DATE: 1998-11-25  
 PRIOR APPLICATION NUMBER: 60/126,794  
 PRIOR FILING DATE: 1999-03-30  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 979  
 TYPE: DNA  
 ORGANISM: mouse  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (44)..(745)  
 NAME/KEY: sig\_peptide  
 LOCATION: (44)..(103)  
 NAME/KEY: V\_region  
 LOCATION: (104)..(172)  
 OTHER INFORMATION: FR1  
 NAME/KEY: V\_region  
 LOCATION: (173)..(205)  
 OTHER INFORMATION: CDR1  
 NAME/KEY: V\_region  
 LOCATION: (206)..(250)  
 OTHER INFORMATION: FR2  
 NAME/KEY: V\_region  
 LOCATION: (251)..(271)  
 OTHER INFORMATION: CDR2  
 NAME/KEY: V\_region







266	GCAGATGGTGGCATCAAGGTTTCAGTGGCAGTGGATCAGGAACAACATATTCTCTCAAG	325
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275	GCAGATGGTGGCGTCAAGGTTTCAGTGGCAGTGGATCAGGAACAACATATTCTCTCAAG	314
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285	ATCAACAGCCTGCAGCCTGAAGATTTTGGAGTTATTACTGTCAACATTTTGGAGTACT	385
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295	ATCAACAGCCTGCAGCCTGAAGATTTTGGAGTTATTACTGTCAACATTTTGGAGTATT	374
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## RESULT 5

S-07-904-074A-1  
Sequence 1, Application US/07904074A  
GENERAL INFORMATION:  
APPLICANT: John E. Shively  
APPLICANT: Rainer Fischer  
APPLICANT: Anna Wu  
APPLICANT: Roy Paxton  
APPLICANT: Y. H. Joy Yang  
TITLE OF INVENTION: Chimeric Anti-CEA Antibody

ZIP: 91010-0269

COMPUTER IDENTIFICATION FORM:

MEDIUM TYPE: 3M Double Density 5 1/4" diskette

COMPUTER: Wang PC

OPERATING SYSTEM: MS-DOS (R) Version 3.30

SOFTWARE: Microsoft (R)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/904,074A

FILING DATE: 19920615

CLASSIFICATION: 530

PRIOR APPLICATION DATA: None

ATTORNEY/AGENT INFORMATION:

NAME: Irons, Edward S.

REGISTRATION NUMBER: 16,541

REFERENCE/DOCKET NUMBER: None

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 785-6938

TELEFAX: (202) 785-5351

TELEX: 440087 LM WSH

```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1041
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single Stranded
; TOPOLOGY: Unknown
; MOLECULE TYPE: Nucleic Acid
; HYPOTHETICAL: Not Applicable
; ANTI-SENSE: Not Applicable
; FRAGMENT TYPE: Not Applicable
; ORIGINAL SOURCE: Synthetically Prepared
; IMMEDIATE SOURCE: Synthetically Prepared
; POSITION IN GENOME: None
; FEATURE: None
; PUBLICATION INFORMATION: None
; US-07-904-074A-1

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Query Match		70.8%;	Score 693.4;	DB 3;	Length 1041;
Best Local Similarity		85.0%;	Prod. No. 4e-86;		
Matches 788; Conservative		0;	Mismatches 136;	Indels 3;	Gaps 1;
QY	56	ACTCAGGTCCTGGCGTTCGCTGCTGTGGCGTTACAGGTGCCAGATGTGACATCCAGATG	115		
Db	46	ACTCAGGTCCTTTGTATACATGTGCTGTGGTTGTCTGTTGATGGAGACATTTGTGCTG	105		
QY	116	ACTCAGTCTCCAGCGTCCTCATCTGTCATCTGTGGAGAAACTGTGCACCATCATCATGTGCA	175		
Db	106	ACCAGTCTCAAAATTCATGTCACATCAGTTGGAGCAGGTCACGCTACCTCGCAAG	165		
QY	176	GCAAGTGGGAATATCAAAATATTATTAGCATGGTATCAGCAGACACAGGGAATAATCTCCT	235		
Db	166	GCCAGTCAAAATGTGCATCTAATGTTGCCCTGGTATCAACAGAAACAGGACAAATCTCCT	225		
QY	236	CAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGTTGCGATCAAGGTTCAAGTGGC	295		
Db	226	AAAGCATGTGATTTACTCGGCATCTACCGTTACAGTGGAGTCCCTGATCGCTTCACAGGC	285		
QY	296	AGTGGATCAGGAACACAATATTCCTCAAGATCAACAGCCTGCAGCCTGAAGATTTGGG	355		
Db	286	AGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGAGTCTTGAAAGACTTGGCA	345		
QY	356	AGTTATTACTCTCAACATTTTTTGGAG---TACTCCGTTACACGTTCCGGAGGGGGACCAAG	412		
Db	346	GAATATTTCTGCAGCAATGTACAGCATATCCTCTATTACGTTTCGCTCGGGGACCAAG	405		
QY	413	CTGGAAATAAACCAGGCTGATGCTGCACCAACTGTATTCATCTTCCACCATCCAGTGAG	472		
Db	406	TTGGAAATAAACCAGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGAG	465		
QY	473	CAGTTAACTCTCGAGGTGCCTCAGTCTGTGTCTTGTGAACAACCTTCAACCCAAAGAC	532		
Db	466	CAGTTAACTCTCGAGGTGCCTCAGTCTGTGTCTTGTGAACAACCTTCAACCCAAAGAC	525		
QY	533	ATCAATGTCAAGTGGAGATTTGATGTCAGTGAACGACGACAAAATGGCGTCTGAAACATTGG	592		
Db	526	ATCAATGTCAAGTGGAGATTTGATGTCAGTGAACGACGACAAAATGGCGTCTGAAACATTGG	585		
QY	593	ACTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCTCTCAGTTGACCAAG	652		
Db	586	ACTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCTCTCAGTTGACCAAG	645		
QY	653	GACGAGTATGACGACATTAACAGCTATACCTGTGAGGGCCACTCAAGAAGCATCAACTTCA	712		
Db	646	GACGAGTATGAACGACATTAACAGCTATACCTGTGAGGGCCACTCAAGAAGCATCAACTTCA	705		
QY	713	CCCATTTCAAGAGCTTCAACAGGAATGAGTGTTAGACAAAGGTCTTGAGACGCCACC	772		
Db	706	CCCATTTCAAGAGCTTCAACAGGAATGAGTGTTAGACAAAGGTCTTGAGACGCCACC	765		
QY	773	ACCAGTCTCCCAGCTCCATCTCTATCTTCCCTTCTAAGTCTTGGAGGCTTCCCCACAGC	832		
Db	766	ACCAGTCTCCCAGCTCCATCTCTATCTTCCCTTCTAAGTCTTGGAGGCTTCCCCACAGC	825		



NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8  
LENGTH: 5711  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
-09-897-006-8

Query Match 64.8%; Score 634.2; DB 33; Length 5711;  
Best Local Similarity 90.8%; Pred. No. 5e-78;  
Matches 675; Conservative 0; Mismatches 60.

61 GGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGTGCAGATCCAGATGACTCA 120  
||||| || |||| |  
2401 GGTCTTCTCTTCTCCTGTGCAGTACTACAGGTGCCACTCCGACATCCAGATGACCACA 2460

121 GTCTCAGCCTCCTATCTCATCTCTGGGAAACTGTCCACATCATATGTCGAGCAAG 180  
|||||  
2461 GTCTCAGCCTCCTATCTCATCTCTGGGAAACTGTCCACATCATATGTCGAGCAAG 2520

[illegible]

241 CCTGGTCTATTCTGCAAAACCTTAGCAGATGCTGCCATCAAGTTCACTGGCAGTGG 300  
|||||  
2581 CCTGGTCTAATGCAAAACCTTAGCAGATGCTGCCATCAAGTTCACTGGCAGTGG 2640

360 ATCAGGAAACAAATATCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA 360  
2641 ATCAGGAACACAATATTTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA 2700

2761 CAACGGGCGTATGTGACCAACTGTATCCATCTTCCACCATCCAGTCAGCAGTTAAC 2820

481 ATCTGGAGGTGCCTCAGTCGTGCTTCTTGAAACAACTTCTACCCCAACACATCATCATCTG 540

2821 ATCTGGAGTGCCTCAGTCGTGCTTCTTGAACAACCTTACCCCAAGACATCAATGT 2880

541 CAAGTGGAGATTGATGGCAGTGAAGCAGCAAAATGGCGTCCCTGAACAGTTGGACTGATCA 600

2881 CAAGTGGAGATTGATGGCAGTTGAACGACAAAATGGCGCTTGAACAGTTGGACTGATCA 2940  
601 GGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCCCTCAGTTTGACCAACGACGAGTA 560

2941 GCACGACAAAGACAGCACCTACAGCATGAGCAGCACCTCACATTGACCAAGGACAGTA 3000

661 TGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCATTCCT 720

721 CAAGAGCTTCAACAGGAATGAGTGTTAGACAAAGGTCCTGAGACGCCACCACCAAGTTC 780  
3001 TGAACGACATACACAGCTATACCTGTGTAGGCCACTCACAAGACATCAACTTCACCCATTGT 3060

3001 CAGAGGCTTCAACAGGAATGAGTGTGAAGAAGCATCGATTTCCCTGGAAATCGCCCTCTC 3120

781 CCCAGCTCCATCCTATCTTCCT 803

3121 TCGAGGCTTCAACAGGAATGAGTGTGAAGAAGCATCGATTTCCCTGGAAATCGCCCTCTC 3240

\*\*\*\*\*  
 JUL 8 09-897-511A-8  
 \*\*\*\*\*

ULT 8  
09-897-511A-8  
Sequence 8, Application US/09897511A  
GENERAL INFORMATION:  
APPLICANT: Bremel, Robert  
APPLICANT: Miller, Linda

```

; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 5711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-8

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Query Match	64.8%;	Score	634.2;	DB 33;	Length 5711;
Best Local Similarity	90.8%;	pred. NO.	5e-78;		
Matches	675;	Conservative	0.	Mismatch	59.

QY	61	GCTCCTGGCGTTGCTGCTGTGGTACAGTGCCAGATGTACATCCAGATCACTCA	120
Db	2401	GCTCTTCCTTCCTTCCTGTCAGTAACATACAGTGTCCACTCCGACATCCAGATGACCAC	2460

121 GTCTCCAGCCTCCCTATCTGCAATCTGGGAGAAACTGTCCACATCACATGTGCGACGAG 180  
|||||  
2461 GTCTCCAGCCTCCCTATCTGCAATCTGGGAGAAACTGTCCACATCACATGTGCGACGAG 2520  
|||||

181 TGGGAATATTCAAATTTATTAGCATGCTATCAGCAGACACAGGAAAATCTCCTCAGT 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2521 TGGGAATATTCAAAATTTATTAGCATGCTATCAGCAGAACAGGAAAATCTCCTCAGT 2580

241 CCTGTCATTTCTGCAAAAACCTTAGCAGATGGTGTGCATCAAGTTTCAGTGGCAGTGG 300  
2581 CCTGTCCTAATATGCAAAAACCTTAGCAGATGGTGTGCATCAAGTTTCAGTGGCAGTGG 2640

[illegible][illegible]

2761 CAAACGGGCTGATGCTGCACCAACTGATCCATCTTCCACCATCCAGTGAGCAGTTAAC 2820

481 ATCTGGAGGTGCCCTCAGTCGTGTGCTCTCTTGAACAACCTTCTACCCCAAGACATCAATGT 540

bb 2821 ATCTGGAGGTGCGTTCGTCCTTGAACAACCTTACCCCAAGACATCAATGT 2880

2y 541 CAAGTGAAGATTGATGGCAGTGAACGACAAAAATGGCGTCCTGAACAGTTCGACTGATCA 600

2381 CAAGTGGAGATTGATGGCAGTGAACGACAAATGGGCTCCTGAACAGTTGGACTGATCA 2940  
601 GGACAGCAAGACAGCAGCTACAGCATGAGCAGCACCTCAGCTTGACCAAGGACGAGTA 660

2941 GGACAGCAAGACAGCACCTACACCATGAGCAGCACCTCACATTGACCAAGGACGAGTA 3000

661 TGAACGACATAACAGCTTATACCTGTGAGGCCACTCAAGACATCAACTTCACCCATTGT 720

3001 TGAACGACATAACAGCTATATCTGTGAGGCCACTCACAAGACATCAACTTTCACCCATTGT 3060

721 CAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAGGTCTCTGAGACGCCACCACCAGCTC 780

5001 CACAGACGCGCCACAGAGAAAGAGTGTAAAGCATCGATTTCCTCGAATTCGCCCCCTCTC 3120

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561 TGAAGCATTAACAGCTATACCTGTGAGGCCACTACAAGACATCAACTTCACCCATTGT 720  
4130 TGAAGCATTAACAGCTATACCTGTGAGGCCACTACAAGACATCAACTTCACCCATTGT 4189  
721 CAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAGGTCTTGAGACGCCACCAACGAGTC 780  
4190 CAAGAGCTTCAACAGGAATGAGTGTGAAGATCGAATTCGCCCTGAATTCGCCCTCTC 4249  
781 CCCAGCTCCATCTCTACTTCCCT 803  
4250 CCTCCCCCCCCCTAACGTTACT 4272

## RESULT 11

07-743-329-4  
Sequence 4, Application US/07743329  
GENERAL INFORMATION:  
APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Emcage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz  
STREET: One Liberty Place - 46th Floor  
City: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07743329  
FILING DATE: 19910917

ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: CARP-0009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 943 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 18..722  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 84..722  
07-743-329-4

Query Match	62.9%	Score 615.6	DB 3	Length 943
Best Local Similarity	84.6%	Pred. No. 2e-75		
Matches 739	Conservative 0	Mismatches 129	Indels 6	Gaps 4
96	CCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCAATCTGTGGGAGAAA	155		
76	CCAGAGGACAAATTTGTTCTACCCAGCTCTCCAGCAATCATGCTGTCATCTCCAGGGGAGA	135		
156	CTGTCCACCATCACATCTCGACCAAGTGGGAATATTCAAAATATTTAGCATATGTTATCAGC	215		
136	AGGTCACCATGACCTGCAGTGCCAGCTCAAGTGT---	192		
216	AGACACAGGGAAATCTCCTCAGCTCTGGTCTATCTGCAAAACCTTTAGCAGATGGTG	275		

[illegible]

## RESULT 12

```

US-08-303-569-4
; Sequence 4, Application US/08303569
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0

```

Version #1.25

CURRENT APPLICATION DATA: US/08/303,569  
 FILING DATE: 17-SEP-1991  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA: US 07/743,329  
 APPLICATION NUMBER: 17-SEP-1991  
 FILING DATE: 17-SEP-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hohenschutz, Liza D.  
 REGISTRATION NUMBER: 33,712  
 REFERENCE/DOCKET NUMBER: CARP-0009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 943 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 18..722  
 NAME/KEY: mat\_peptide  
 LOCATION: 84..722

Query Match 62.9%; Score 615.6; DB 7; Length 943;  
 Best Local Similarity 84.6%; Pred. No. 2e-75;  
 Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;

96	CCAGATGTGACATCCAGATGACTCAGTCTCCAGCTCCCTATCTGCAATCTGCGGAGAA	155
76	CCAGAGGACAAATTTCTCACCAGTCCAGCAATCATCTGCAATCTCCAGGGAGA	135
156	CTGTCACCATCAGATGTCGAGCAATGGAATATTCAAAATTTATTAGCATGGTATCAGC	215
136	AGGTACCATCAGCTGCGAGTCCAGCTCAAGTGT---AAGTTACATGACTGGTACCAGC	192
216	AGACACAGGGAAATCTCTCAGCTCTCTGCTATCTGCAAAACCTTAGCAGATGGTG	275
193	AGAATGAGGACCTCCCTCCCAAGATGATTTATGACATCCCAACTGGCTTCTGGAG	252
276	TGCCATCAAGTTTCACTGGGAGTGGATCAGGAAACAATATTTCTCAAGATCAACAGCC	335
253	TCCCTGCTCACTTCAGGGGAGTGGTCTGGGACCTCTTACTCTCTCAATCAAGCGCA	312
336	TGCAGCTGAGATTTTGGGAGTTATTACTGTCACATTTTGGAGTACTCCGTACAGCT	395
313	TGGAGCTGAAGATCTGCACTTATTACTTATTCAGCAGTGGAGTAGTACACCATCAGCT	372
396	TGGAGGGGGGACCAAGCTGGAATAAAGGGGCTGATGCTGCACCACTGATCCATCT	455
373	TGGGCTCGGGGCAAGTTGGAAATTAACCGGCTGATGATGACCACTGATCCATCT	432
456	TCCCACTCCAGTGAAGAGTTAAACATCTGGAGGTGCTCAGTCTGCTGCTTCTTGAACA	515
433	TCCCACTCCAGTGAAGAGTTAAACATCTGGAGGTGCTCAGTCTGCTGCTTCTTGAACA	492
516	ACTTCTACCCCAAGACATCAATGTCAGTGAAGATTTGTCAGTGAACGACCAAAATG	575
493	ACTTCTACCCCAAGACATCAATGTCAGTGAAGATTTGTCAGTGAACGACCAAAATG	552
576	GGTCTCTGAACAGTTGGATGATCAGGACGACCAAGACAGCCTACAGCATGACGACGA	635
553	GGGTCTCTGAACAGTTGGATGATCAGGACGACCAAGACAGCCTACAGCATGACGACGA	612
636	CCCTCAGTTGACCAAGGAGTATGACGACATTAACAGCTATATCTGTGAGGCCACTC	695
613	CCCTCAGTTGACCAAGGAGTATGACGACATTAACAGCTATATCTGTGAGGCCACTC	672

696 ACAAGACATCAACTTCACCATTTGTCAAGAGCTTCAACAGGAATGAGTGTAGACAAA 755  
 673 ACAAGACATCAACTTCACCATTTGTCAAGAGCTTCAACAGGAATGAGTGTAGACAAA 732  
 756 GGTCTTGAGAGCGCACCAACAGCTCCCGAGCTCCATCTATCTTCCCTTCAAGGTCTTG 815  
 733 GGTCTTGAGAGCGCACCAACAGCTCCCGAGCTCCATCTATCTTCCCTTCAAGGTCTTG 791  
 816 GAGCTTCCCGACCAAGCGAGCTACCACTGTGGGTGCTCCAAACCTCCCGCCACCTCC 875  
 792 GAGCTTCCCGACCAAGCG-CTTACCAGTGTGGGTGCTCTAAACCTCCT-CCACCTCC 849  
 876 TTCT 935  
 850 TTCT 909  
 936 TAAAGTGAGTCTTTGGCAAAAAA 969  
 910 TAAAGTGAGTCTTTGGCTTGA 943

RESULT 13  
 US-08-485-686-4  
 ; Sequence 4, Application US/08485686  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adair, John R.  
 ; APPLICANT: Athwal, Diljeet S.  
 ; APPLICANT: Emage, John S.  
 ; TITLE OF INVENTION: Humanised Antibodies  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/485,686  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/743,329  
 ; FILING DATE: 17-SEP-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hohenschutz, Liza D.  
 ; REGISTRATION NUMBER: 33,712  
 ; REFERENCE/DOCKET NUMBER: CARP-0009  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 943 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 18..722  
 ; FEATURE:  
 ; NAME/KEY: mat\_peptide  
 ; LOCATION: 84..722  
 ; US-08-485-686-4

Query Match 62.9%; Score 615.6; DB 8; Length 943;  
 Best Local Similarity 84.6%; Pred. No. 2e-75;





576 GCGTCTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCAGCTACAGCATGAGCAGCA 635  
|||||  
553 GCGTCTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCAGCTACAGCATGAGCAGCA 612  
|||||  
636 CCCTCAGCTTGACCAAGGACGAGTATGAACAGACATACAGCTATACCTGTGAGGCCACTC 695  
|||||  
613 CCCTCAGCTTGACCAAGGACGAGTATGAACAGACATACAGCTATACCTGTGAGGCCACTC 672  
|||||  
696 ACAAGACATCAACTTCAACCATTTGCTCAAGAGCTTCAACAGAGATGAGTGTAGAGACAAA 755  
|||||  
673 ACAAGACATCAACTTCAACCATTTGCTCAAGAGCTTCAACAGAGATGAGTGTAGAGACAAA 732  
|||||  
756 GGTCTGAGAGCGGACACAGCTCCCGAGCTCCATCTATCTTCCCTTCAAGGTCTTG 815  
|||||  
733 GGTCTGAGAGCGGACACAGCTCCCGAGCTCCATCTATCTTCCCTTCAAGGTCTTG 791  
|||||  
816 GAGCTTCCCAACAGGACCTACCACTGTGGGTGCTCCAAACCTCCCTCCCAACCTCC 875  
|||||  
792 GAGCTTCCCAACAGGACCTACCACTGTGGGTGCTCCAAACCTCCCTCCCAACCTCC 849  
|||||  
876 TTCT 935  
|||||  
850 TTCT 909  
|||||  
936 TAAAGTGAGTCTTTTGCAAAAAA 969  
|||||  
910 TAAAGTGAGTCTTTTGCAAAAAA 943  
|||||

## -08-846-658B-4

Sequence 4, Application US/08846658B

## GENERAL INFORMATION:

APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Entage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/846,658B  
FILING DATE: 01-MAY-1997  
CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yanko  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CARP-0057

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439

## INFORMATION FOR SEQ ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 943 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 18..722

FEATURE:

NAME/KEY: mat\_peptide

; LOCATION: 84..722

US-08-846-658B-4

## Query Match

Best Local Similarity 84.6%; Score 615.6; DB 12; Length 943;

Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;

QY 96 CCAGATGTGACATCCAGATGACTCAGTCTCCAGCTCCCTATCTGCAATCTGTGGGAGAAA 155  
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DB 76 CCAGAGACAAATTTGTTCTCACCAGTCTCCAGCAATCATCTCTGCAATCTCCAGGGAGA 135  
|||||  
QY 156 CTGTCCACATCAATGTCCGAGCAAGTGGGAATATTCAAAATTTATTAGCATGGTATCAGC 215  
|||||  
DB 136 AGTTCACCATGACCTGCGAGTCCAGCTCAAGTGT---AAGTTACATGAACCTGGTACCAGC 192  
|||||  
QY 216 AGACACAGGGAATCTCCTCAGCTCCTGGTCTATTTCTGCAAAACCTTAGCATGATGGT 275  
|||||  
DB 193 AGAAGTCAGGCACCTCCCAAGATGGATTTATGACACATCCAACTGGCTTCTGGAG 252  
|||||  
QY 276 TGCCATCAAGGTTTCAGTGGCAGTGGATCAGGACACACAATATTTCTCAAGATCAACAGCC 335  
|||||  
DB 253 TCCCTGTCTCACTTCAGGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCGSCA 312  
|||||  
QY 336 TGCAGCCTGAAGATTTTGGGAGTTATTACTCTCAACAATTTTGGAGTACTCCGTACAGCT 395  
|||||  
DB 313 TGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCATTTCAGCT 372  
|||||  
QY 396 TCGGAGGGGGACCAAGCTGGAATATAAACCAGGCTGATGCTGCACCAACTGTATCCATCT 455  
|||||  
DB 373 TCGGCTCGGGACAAAGTTGGAATATAAACCAGGCTGATGCTGCACCAACTGTATCCATCT 432  
|||||  
QY 456 TCCACACATCCAGTCCAGTGGAGTGAACATCTGGAGTGGCTCAGTCTGTCTTGAACA 515  
|||||  
DB 433 TCCACACATCCAGTCCAGTGGAGTGAACATCTGGAGTGGCTCAGTCTGTCTTGAACA 492  
|||||  
QY 516 ACTTCTACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAAATG 575  
|||||  
DB 493 ACTTCTACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAAATG 552  
|||||  
QY 576 GCGTCTGAACAGTTGGACTGATCAGGACAGCAAGACAGACACCTACAGCATGAGCAGCA 635  
|||||  
DB 553 GCGTCTGAACAGTTGGACTGATCAGGACAGCAAGACAGACACCTACAGCATGAGCAGCA 612  
|||||  
QY 636 CCCTCAGCTTGACCAAGGACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTC 695  
|||||  
DB 613 CCCTCAGCTTGACCAAGGACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTC 672  
|||||  
QY 696 ACAAGACATCAACTTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAA 755  
|||||  
DB 673 ACAAGACATCAACTTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAA 732  
|||||  
QY 756 GGTCTGAGAGCGCCACCAAGCTCCAGCTCCCAAGCTCCATCTCTCCCTTCTAAGGTCTTG 815  
|||||  
DB 733 GGTCTGAGAGCGCCACCAAGCTCCAGCTCCCAAGCTCCATCTCTCTCCCTTCTAAGGTCTTG 791  
|||||  
QY 816 GAGGCTTCCCAACAGGACCTACCACTGTGGGTGCTCCAAACCTCTCCCAACCTCC 875  
|||||  
DB 792 GAGGCTTCCCAACAGGACCTACCACTGTGGGTGCTCCAAACCTCTCCCAACCTCC 849  
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QY 876 TTCT 935  
|||||  
DB 850 TTCT 909  
|||||  
QY 936 TAAAGTGAGTCTTTTGCAAAAAA 969  
|||||  
DB 910 TAAAGTGAGTCTTTTGCAAAAAA 943  
|||||

Search completed: June 24, 2003, 00:11:44

Job time : 2455.36 secs





61 GGTCTCGGGTGTCTGCTGTGGCTTACAGTGCAGATGACATCCAGATGACTCA 120  
 3530 GGTCTTCTCTTCTCTGTCAGTACTACAGTGTCCACTCCGACATCCAGATGACCCA 3589  
 121 GTCCTCAGCTCCCTATCTGATCTGTGGAGAACTGTCAACATCAGATGTCGAGCAAG 180  
 3590 GTCCTCAGCTCCCTATCTGATCTGTGGAGAACTGTCAACATCAGATGTCGAGCAAG 3649  
 181 TGGGAATATTCAGAAATATTTAGCATGGTATCAGCAGACACAGGAAATCTCCTCAGCT 240  
 3650 TGGGAATATTCAGAAATATTTAGCATGGTATCAGCAGACACAGGAAATCTCCTCAGCT 3709  
 241 CTTGTCTATTCGAAAACTTACGAGATGGTGTGCGATCAAGGTTCAAGTGGCAGTGG 300  
 3710 CTTGTCTATTCGAAAACTTACGAGATGGTGTGCGATCAAGGTTCAAGTGGCAGTGG 3769  
 301 ATCAGGAACAATATTTCTCAAGATCAACAGCTGTGAGGAGGAGCAAGCTGGAAT 360  
 3770 ATCAGGAACAATATTTCTCAAGATCAACAGCTGTGAGGAGGAGCAAGCTGGAAT 3829  
 361 TTACTGTCAACATATTTTGGAGTACTCCGTCAGCTGTGAGGAGGAGCAAGCTGGAAT 420  
 3830 TTACTGTCAACATATTTTGGAGTACTCCGTCAGCTGTGAGGAGGAGCAAGCTGGAAT 3889  
 421 AAAAGGGCTCATCTGCACCACTGTATCCATCTTCCACATCCAGTGGAGCTTAAC 480  
 3890 AAAAGGGCTCATCTGCACCACTGTATCCATCTTCCACATCCAGTGGAGCTTAAC 3949  
 481 ATCTGGAGTGCCTCAGTCGCTGTGCTTCTGAAACAATTTTACCCCAAGACATCAATGT 540  
 3950 ATCTGGAGTGCCTCAGTCGCTGTGCTTCTGAAACAATTTTACCCCAAGACATCAATGT 4009  
 541 CAAGTGAAGATTGATGGCAGTGAACGACAAATTTGCGTCTGAAACAATTTTACCCCAAGACATCAATGT 600  
 4010 CAAGTGAAGATTGATGGCAGTGAACGACAAATTTGCGTCTGAAACAATTTTACCCCAAGACATCAATGT 4069  
 601 GGACAGAAAGACAGCAGCTACAGCATGAGCAGACCCCTCAGTGTGACCAAGGAGGAGTA 660  
 4070 GGACAGAAAGACAGCAGCTACAGCATGAGCAGACCCCTCAGTGTGACCAAGGAGGAGTA 4129  
 661 TGAACGACATTAACAGCTATACCTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 720  
 4130 TGAACGACATTAACAGCTATACCTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 4189  
 721 CAAGAGCTTCAACAGGAATGAGTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 780  
 4190 CAAGAGCTTCAACAGGAATGAGTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 4249  
 781 CCCAGCTCCATCTCTTCTTCCCT 803  
 4250 CCTCCCCCCCCCTTACCTTACT 4272

RESULT 4

S-09-897-006-13  
 Sequence 13, Application US/09897006  
 Patent No. US200201067291  
 GENERAL INFORMATION:  
 APPLICANT: Bleck, Gregory  
 TITLE OF INVENTION: Expression Vectors  
 FILE REFERENCE: GALA-06415  
 CURRENT APPLICATION NUMBER: US/09/897, 006  
 CURRENT FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 60/215,851  
 PRIOR FILING DATE: 2000-07-03  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 13  
 LENGTH: 6255  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic

US-09-897-006-13

Query Match 64.8%; Score 634.2; DB 10; Length 6255;  
 Best Local Similarity 90.8%; Pred. No. 1.4e-156;  
 Matches 675; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

61 GGTCTCGGGTGTCTGCTGTGGCTTACAGTGCAGATGACATCCAGATGACTCA 120  
 3530 GGTCTTCTCTTCTCTGTCAGTACTACAGTGTCCACTCCGACATCCAGATGACCCA 3589  
 121 GTCCTCAGCTCCCTATCTGATCTGTGGAGAACTGTCAACATCAGATGTCGAGCAAG 180  
 3590 GTCCTCAGCTCCCTATCTGATCTGTGGAGAACTGTCAACATCAGATGTCGAGCAAG 3649  
 181 TGGGAATATTCAGAAATATTTAGCATGGTATCAGCAGACACAGGAAATCTCCTCAGCT 240  
 3650 TGGGAATATTCAGAAATATTTAGCATGGTATCAGCAGACACAGGAAATCTCCTCAGCT 3709  
 241 CTTGTCTATTCGAAAACTTACGAGATGGTGTGCGATCAAGGTTCAAGTGGCAGTGG 300  
 3710 CTTGTCTATTCGAAAACTTACGAGATGGTGTGCGATCAAGGTTCAAGTGGCAGTGG 3769  
 301 ATCAGGAACAATATTTCTCAAGATCAACAGCTGTGAGGAGGAGCAAGCTGGAAT 360  
 3770 ATCAGGAACAATATTTCTCAAGATCAACAGCTGTGAGGAGGAGCAAGCTGGAAT 3829  
 361 TTACTGTCAACATATTTTGGAGTACTCCGTCAGCTGTGAGGAGGAGCAAGCTGGAAT 420  
 3830 TTACTGTCAACATATTTTGGAGTACTCCGTCAGCTGTGAGGAGGAGCAAGCTGGAAT 3889  
 421 AAAAGGGCTCATCTGCACCACTGTATCCATCTTCCACATCCAGTGGAGCTTAAC 480  
 3890 AAAAGGGCTCATCTGCACCACTGTATCCATCTTCCACATCCAGTGGAGCTTAAC 3949  
 481 ATCTGGAGTGCCTCAGTCGCTGTGCTTCTGAAACAATTTTACCCCAAGACATCAATGT 540  
 3950 ATCTGGAGTGCCTCAGTCGCTGTGCTTCTGAAACAATTTTACCCCAAGACATCAATGT 4009  
 541 CAAGTGAAGATTGATGGCAGTGAACGACAAATTTGCGTCTGAAACAATTTTACCCCAAGACATCAATGT 600  
 4010 CAAGTGAAGATTGATGGCAGTGAACGACAAATTTGCGTCTGAAACAATTTTACCCCAAGACATCAATGT 4069  
 601 GGACAGAAAGACAGCAGCTACAGCATGAGCAGACCCCTCAGTGTGACCAAGGAGGAGTA 660  
 4070 GGACAGAAAGACAGCAGCTACAGCATGAGCAGACCCCTCAGTGTGACCAAGGAGGAGTA 4129  
 661 TGAACGACATTAACAGCTATACCTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 720  
 4130 TGAACGACATTAACAGCTATACCTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 4189  
 721 CAAGAGCTTCAACAGGAATGAGTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 780  
 4190 CAAGAGCTTCAACAGGAATGAGTGTGAGGAGCACTCAAGACATCAATTTCAACCATTTGT 4249  
 781 CCCAGCTCCATCTCTTCTTCCCT 803  
 4250 CCTCCCCCCCCCTTACCTTACT 4272

RESULT 5

US-09-795-515-4  
 ; Sequence 4, Application US/09795515  
 ; Publication No. US20030039645A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adair, John R.  
 ; APPLICANT: Athwal, Diljeet S.  
 ; APPLICANT: Emage, John S.  
 ; TITLE OF INVENTION: Humanised Antibodies  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia

us-09-770-916-3.rnpb

576	QY	GGCTCTGAACAGTTGGACTGATCAGAGACAGAAACAGCACCTTACAGCATCAGCAGCA	633
553	Db	GGTCTTGAACAGTTGGACTGATCAGGACAGAAAGACAGCACTTACAGCATGAGCAGCA	612
636	QY	CCCTCACGTTTGACCAAGGACGAGTATGAACGACATATACAGCTATACCTGTGAGGCCACTC	695
613	Db	CCCTCACGTTGACCAAGGACGAGTATGAAGGACATATACAGCTATACCTGTGAGGCCACTC	672
696	QY	ACAAGACATCAACTTCACCCATTGTCGAAGAGCTTCAACAGGAATGAGTGTAGAGACAAA	755
673	Db	ACAAGACATCAACTTCACCCATTGTCGAAGAGCTTCAACAGGAATGAGTGTAGAGACAAA	732
756	QY	GGTCTTGAGAGCGCCACACAGCTCCCCAGCTCCATCCTATCTTCCTTCTTAAGGTCCTTG	815
733	Db	GGTCTTGAGAGCGCCACACAGCTCCCAGCTCCATCTTCCTTCTTAAGGTCCTTG	791
816	QY	GAGGCTTCCCNACAGCAGCACTACCACCTGTTGCGGTGCTCCAACCTCTCCACCACTCC	875
792	Db	GAGGCTTCCCNACAGCAGCTAACACCTGTTGCGGTGCTCTAAACCTCTCTCCACCTCC	849
876	QY	TTCTCCTCCTCCTCCCTTTCCTTGGCTTTTATCATGTATAATTTGCAGAAAAATATTCAA	935
850	Db	TTCTCCTCCTCCTCCCTTTCCTTGGCTTTTATCATGTATAATTTGCAGAAAAATATTCAA	909
936	QY	TAAAGTGAGTCTTTTGCAGAAAAAATAAAAAA	969
910	Db	TAAAGTGAGTCTTTTGCCTTTGAAAAAATAAAAAA	943

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RESULT 6
US-09-903-327A-3
; Sequence 3, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903, 327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-3

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; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
; US-09-903-327A-3

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; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
; US-09-903-327A-3

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; CURRENT APPLICATION NUMBER: 09/07-07-10
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
; US-09-903-327A-3

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1  PRIOR APPLICATION NUMBER: 09/613,017
2
3  PRIOR FILING DATE: 2000-07-10
4
5  NUMBER OF SEQ ID NOS: 33
6
7  SOFTWARE: FastSeq for Windows Version 4.0
8
9  SEQ ID NO 3
10
11     LENGTH: 831
12
13     TYPE: DNA
14
15     ORGANISM: Mouse
16
17     FEATURE:
18
19     NAME/KEY: CDS
20
21     LOCATION: (13)...(726)
22
23     OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
24
25     US-09-903-327A-3

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; PRIOR FILING DATE: 2000-07-10
;
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 3
;   LENGTH: 831
;   TYPE: DNA
;   ORGANISM: Mouse
;
; FEATURE:
;
;   NAME/KEY: CDS
;   LOCATION: (13)...(726)
;   OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
;
; OS-09-903-327A-3
;

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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 3
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Mouse
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
;
; OS=09-903-327A-3

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; SEQ ID NO 3
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
; OS: 09-903-327A-3

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? LENGTH: 831
? TYPE: DNA
? ORGANISM: Mouse
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (13)...(726)
? OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
? DS-03-903-327A-3

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1  TITLE: DAV-1
2  REF. ID: A60000
3  ORGANISM: Mouse
4  FEATURE:
5  NAME/KEY: CDS
6  LOCATION: (13)...(726)
7  OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
8  DTG: 08-903-327A-3

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
; TS-09-903-327A-3
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; NAME/KEY: CDS
; LOCATION: (13)...(726)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-3

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OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody  
US-09-903-327A-3

US-99-903-327A-3

Query Match 54.6%; score 535; DB 9; Length 831;

Best Local Similarity	80.4%	pred. No. 7.2e-131;	Indels 12;	Gaps 1
Mismatches	0	Mismatches 145;		
Conservative				

Matches	644;	Conservative	0;	Mismatches	145;	Indels	22;	5'-P
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QY  
38 ACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGCTGCTGCTTACAGGTGCC 97

7 ACCCGCATCCACACACACACAATCCTGGTATGGGTGCTGCTGCTGCCAGGCTCC 66

DB / ACCGCCAATGGAGACAGACACACATCCACGCTATCGGCCTCCTTTC

QY 98 AGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACT 15

67 ACTGGTGACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGG 128

07 ACTGTCGCHTATCTCCTCGCCGGAGTTGGCTT

\*\*\*\*\*CCCA CCG

QY  
158 GTCACCATCACATGTCGAGCAAGTGGGAATATTCAA-----AATTATTAGCA 209

db  
127 GCCACCATCTCCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAAC 18

[illegible]

QY 206 TGGTATCAGCAGACACAGGGAAATCTCCTCAGCTCCCTGGTCTATTCTGCAAAATACCTTA 20











Query Match	Best Local Similarity	Score	DB	Length
Matches 531; Conservative	0;	Mismatches 125; Indels 6; Gaps 2;		
104	GACATCCAGATGACTCAGTCTCCAGGCTCCCTATCTGCTATCTGGGAGAACTGTGCACC	163		
3800	GACATTGTGCTGACACAATCTCCAGCAATCATCTGTCATCTCCAGGGAGAGGTCACC	3859		
164	ATCACATGTCGAGCAAGTGGGAATATTCAAAAATTATTAGCATGGTATCAGCAGACACAG	223		
3860	ATGACCTGCACTGCCACCTCAAGTGT---AAGTTACATACACTGGTACCAGCAGAGTCA	3916		
224	GAAATCTCCTCAGTCTGCTGTATTCTTGC AAAACCTTTAGCAGATGGTGTGCCATCA	283		
3917	GGCAGCTCCCCAAAAGATGGATTATGACATCCAAACTGCGCTTCTGGAGTCCCTGCT	3976		
284	AGGTTTCAGTGGCAGTGGATCAGGACACAATATTCTCAAGATCAACAGCCTGCAGCCT	343		
3977	CGCTTCAGTGGCAGTGGGTCTGGGACCTCTCACTCTCACACTCAGCAGATGGAGGCT	4036		
344	GAAGATTTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTACAGTTTCGGAGGG	403		
4037	GAAGATGCTGCCACTATTACTGCGCAGCA---GTGGGTAGTTACCTCACGTTTCGGTGGG	4093		
404	GGGACCAAGCTGGAAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA	463		
4094	GGGACCAAGCTGGAGCTGAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA	4153		
464	TCCAGTGAGCAGTTAACATCTGGAGTGGCTCAGTCTGTGCTTCTTGAACAACCTTCTAC	523		
4154	TCCAGTGAGCAGTTAACATCTGGAGTGGCTCAGTCTGTGCTTCTTGAACAACCTTCTAC	4213		
524	CCCAAGACATCAATGTCAAGTGGGAAGATTGATGCGAGTGAACGACAAAATGCGCTCTG	583		
4214	CCCAAGACATCAATGTCAAGTGGGAAGATTGATGCGAGTGAACGACAAAATGCGCTCTG	4273		
584	AACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGATGAGCAGCACCTCAGG	643		
4274	AACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGATGAGCAGCACCTCAGG	4333		
644	TTGACCAAGGACGAGTATGAACGACATTAACAGCTTATACCTGTGAGGCCACCTCAGG	703		
4334	TTGACCAAGGACGAGTATGAACGACATTAACAGCTTATACCTGTGAGGCCACCTCAGG	4393		
704	TCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTCTTATAGACCAAGGTCCTGA	763		
4394	TCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTCTTATAGGCGAGATCTCGA	4453		

RESULT 15  
US-09-897-006-11  
; Sequence 11, Application US/09897006  
; Patent No. US2020106729A1  
; GENERAL INFORMATION:

RESULT 14  
3-09-897-511A-11  
Sequence 11, Application US/09897511A  
Publication No. US20030092882A1  
GENERAL INFORMATION:  
APPLICANT: Bremel, Robert  
APPLICANT: Miller, Linda  
APPLICANT: Bleck, Gregory  
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors

Tue Jul 1 18:41:02 2003

APPLICANT: Bleck, Gregory  
 TITLE OF INVENTION: Expression Vectors  
 FILE REFERENCE: GALA-06415  
 CURRENT APPLICATION NUMBER: US/09/897,006  
 CURRENT FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 60/215,851  
 PRIOR FILING DATE: 2000-07-03  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 11  
 LENGTH: 5691  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 -09-897-006-11

Query Match	43.98;	Score 430;	DB 10;	Length 5691;
Best Local Similarity	80.2%;	Pred. No. 7e-103;		
Matches	531;	Conservative 0;	Mismatches 125;	Indels 6; Gaps 2;

104	GACATCCAGATGACTCAGTCTCCAGCCCTCCCTATCTGCATCTGTGGGAGAACTGTCAAC	163
3800	GACATTTGTCTGACACAAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAAC	3859
164	ATCACATGTCGAGCAAGTGGGAATATTCAAAATTTATTAGCATGGTATCAGCAGACACAG	223
3860	ATGACCTGCAGTGCACCTCAAGTGT---AAGTTACATACACTGTTACCCAGCAGAAAGTCA	3916
224	GGAAATCTCTCAGCTCCTCGTCTATTCTCTCAAAACCTTAGCAGATGGTGGCCATCA	283
3917	GGCACCCTCCCCAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCT	3976
284	AGGTTCACTGGCAGTGGATCAGGACACAAATATTCTCTCAAGATCAACAGGCTGCAGGCT	343
3977	CGCTTCACTGGCAGTGGGTCTGGGACCTCTCTCTCTCTCAGCTCAGCAGCATGGAGGCT	4036
344	GAAGATTTTGGGAGTTATTACTGTCAACATTTTGGAGTACTTCCGTACACGTTGCGAGGG	403
4037	GAAGATGCTGCCACTTATTACTGCCAGCA---GTGGGGTAGTTACCTCAGGTTGCGTGGC	4093
404	GGGACCAAGCTGGAATAAAAGGGGCTGATGTCGACCAACTGTATCCATCTTCCACCA	463
4094	GGGACCAAGCTGGAGCTGAACGGGCTGATGTCGACCAACTGTATCCATCTTCCACCA	4153
464	TCCATGTAGCAGTTAACATCTGGAGTGCTCAGTCGTCGTCCTTCTTGAACAACCTCTAC	523
4154	TCCAGTGCAGCAGTTAACATCTGGAGTGCTCAGTCGTCGTCCTTCTTGAACAACCTCTAC	4213
524	CCCAAGACATCAATGTCAAGTGGAGATTTGATGGCAGTGAACGACAAATGGCGTCTTG	583
4214	CCCAAGACATCAATGTCAAGTGGAGATTTGATGGCAGTGAACGACAAATGGCGTCTTG	4273
584	AACAGTTGGAGTGTATCAGGACAGCAAGAGCAGCAGCTACAGCATGAGCAGCAGCAGCAG	643
4274	AACAGTTGGAGTGTATCAGGACAGCAAGAGCAGCAGCTACAGCATGAGCAGCAGCAGCAG	4333
644	TTGACCAAGGAGCAGTGTATGAGCAGCATACAGCTATACCTGTGAGGCCACTCACAAGACA	703
4334	TTGACCAAGGAGCAGTGTATGAGCAGCATACAGCTATACCTGTGAGGCCACTCACAAGACA	4393
704	TCAACTTCAACCATTTGAGCAGCTTCAACAGGATGAGTGTAGAGACAAAGTCCCTGA	763
4394	TCAACTTCAACCATTTGAGCAGCTTCAACAGGATGAGTGTAGAGACAAAGTCCCTGA	4453
764	GA 765	
4454	CA 4455	

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:18:11 ; Search time 51.8675 Seconds  
(without alignments)  
5788.524 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 acaccccttgctggagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*

5: /cgn2\_6/ptodata/1/ina/PCFUS\_COMB.seq: \*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Query	Score	Match	Length	ID	Description
1	708.6	72.4	751	5	PCT-US94-07659-3	Sequence 3, Appli
2	667.6	68.2	927	2	US-07-690-192-1	Sequence 1, Appli
3	650.6	66.5	940	1	US-08-353-400-24	Sequence 24, Appli
4	626	63.9	1644	2	US-08-792-824-11	Sequence 11, Appli
5	626	63.9	1672	2	US-08-792-824-2	Sequence 2, Appli
6	626	63.9	4435	2	US-08-792-824-1	Sequence 1, Appli
7	622.8	63.6	1632	2	US-08-792-824-8	Sequence 8, Appli
8	615.6	62.9	943	2	US-08-303-569B-4	Sequence 4, Appli
9	615.6	62.9	943	2	US-08-116-247-4	Sequence 4, Appli
10	597.2	61.0	1641	2	US-08-792-824-5	Sequence 5, Appli
11	517.2	52.8	642	2	US-08-634-783A-2	Sequence 2, Appli
12	517.2	52.8	642	2	US-09-070-817-2	Sequence 2, Appli
13	509.6	52.1	652	2	US-08-737-129A-7	Sequence 7, Appli
14	485.8	49.6	5238	6	5453363-1	Patent No. 5453363
15	482.6	49.3	633	4	US-09-170-769A-7	Sequence 7, Appli
16	460.2	47.0	1066	1	US-08-157-101A-4	Sequence 4, Appli
17	459.2	46.9	714	3	US-09-192-545-3	Sequence 3, Appli
18	458.8	46.9	723	5	PCT-US94-14106-56	Sequence 56, Appli
19	449.4	45.9	732	2	US-08-860-882A-26	Sequence 26, Appli
20	449.4	45.9	732	4	US-09-423-439-57	Sequence 57, Appli
21	449.4	45.9	732	4	US-09-011-769A-22	Sequence 22, Appli
22	436.8	44.6	648	6	5455030-4	Patent No. 5455030
23	432.8	44.2	646	2	US-08-737-129A-3	Sequence 3, Appli
24	432	44.1	3819	4	US-09-042-353-393	Sequence 393, App
25	432	44.1	3819	4	US-08-758-417A-243	Sequence 243, App
26	422.2	43.1	645	4	US-09-170-769A-3	Sequence 3, Appli
27	411	42.0	723	5	PCT-US94-14106-60	Sequence 60, Appli

28	407.6	41.6	19040	4	US-09-343-485A-3	Sequence 3, Appli
29	393.8	40.2	726	4	US-08-487-283A-9	Sequence 9, Appli
30	389.8	39.8	1443	2	US-08-403-853-19	Sequence 19, Appli
31	384.4	39.3	705	1	US-08-488-376-16	Sequence 16, Appli
32	384.4	39.3	705	2	US-08-634-223-16	Sequence 16, Appli
33	384.4	39.3	705	2	US-08-634-224-16	Sequence 16, Appli
34	384.4	39.3	705	2	US-08-634-400-16	Sequence 16, Appli
35	384.4	39.3	705	2	US-08-635-878-16	Sequence 16, Appli
36	384.4	39.3	705	2	US-08-770-057-16	Sequence 16, Appli
37	384.4	39.3	705	4	US-09-335-697B-16	Sequence 16, Appli
38	384.4	39.3	705	4	US-09-335-697B-16	Sequence 16, Appli
39	382.6	39.1	931	3	US-09-049-672A-19	Patent No. 5219996
40	378.2	38.6	420	6	5219996-18	Sequence 5, Appli
41	376.4	38.4	472	2	US-08-579-940-5	Sequence 15, Appli
42	365.6	37.3	711	4	US-08-487-283A-15	Sequence 18, Appli
43	365.2	37.3	708	1	US-08-488-376-18	Sequence 18, Appli
44	365.2	37.3	708	2	US-08-634-223-18	Sequence 18, Appli
45	365.2	37.3	708	2	US-08-634-224-18	Sequence 18, Appli

#### ALIGNMENTS

RESULT 1  
PCT-US94-07659-3  
; Sequence 3, Application PC/TUS9407659  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurler, Mark  
; APPLICANT: Jackson, Jeffrey R.  
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta  
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corp.  
; ADDRESSEE: Intellectual Property  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07659  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/090,534  
; FILING DATE: 09-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50171-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 270-5024  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 751 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS



[illegible]

### RESULT 3

US-08-353-400-24  
; Sequence 24, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 940 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
S-08-353-400-24

	Query Match	66.5%	Score 650.6;	DB 1;	Length 940;
	Best Local Similarity	83.8%;	Pred. No. 1.6e-147;		
	Matches 780;	Conservative 0;	Mismatches 129;	Indels 22;	Gaps 3;
y	39 CAGTCATCAGTGTGCTCACTCAGCTCTCGGCTGCTGCTGCTGCCTACAGGTGCCA	98			
b	5 CCGCAGTGAGTTACAGCCCGAGGCTTTATATTGCTGCTATCGGTATCTGGAACTT	64			
y	99 GATGTGACATCCAGATGACTCAGTCTCCAGCTCCCTATCTGCATCTGTGGGAGAAGTC	158			
b	65 GTGGGGACATTGATGATTCAGTCTCATCTCCCTCCCTGGCTGTGTCAAGGAGAGAACG	124			
y	159 TCACCATCACATGTCGAGCAAGTGGGNATTC-----AAAATTATT	200			

[illegible]

## RESULT 4

US-08-792-824-11  
; Sequence 11, Application US/08792824  
; Patent No. 5932449  
; GENERAL INFORMATION:  
; APPLICANT: EMANUEL, PETER A.  
; APPLICANT: BURANS, JAMES P.  
; APPLICANT: VALDES, JAMES J.  
; APPLICANT: MOHYEE, ELDEFRAWI E.  
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: U.S. Army Chemical and Biological Defense  
; ADDRESS: Command  
; STREET: Office of the Chief Counsel, Bldg E4435  
; CITY: Aberdeen Proving Ground  
; STATE: MD





GENERAL INFORMATION:  
APPLICANT: EMANUEL, PETER A.  
APPLICANT: BURANS, JAMES P.  
APPLICANT: VALDES, JAMES J.  
APPLICANT: MOHYEE, ELDEFRAWI E.  
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: U.S. Army Chemical and Biological Defense  
ADDRESSER: Command  
STREET: Office of the Chief Counsel, Bldg E4435  
CITY: Aberdeen Proving Ground  
STATE: MD  
COUNTRY: U.S.  
ZIP: 21010-5423  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,824  
FILING:

ZIP: 21010-5423  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/792,824  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Biffoni, U. J.  
 REGISTRATION NUMBER: 39,908  
 REFERENCE/DOCKET NUMBER: DAM 431-96  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 410-671-1158  
 TELEFAX: 410-671-2534  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4435 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Mus musculus  
 STRAIN: BALB/c  
 IMMEDIATE SOURCE:  
 CLONE: Clone phist 5  
 08-792-824-1

Very Match	63.9%;	Score 626;	DB 2;	Length 4435;
Best Local Similarity	92.9%;			
atches 656: Conservative				

RESULT 6  
S-08-792-824-1  
Sequence 1, Appendix  
Patent No. 593



Patent No. 5859205  
GENERAL INFORMATION:  
APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
APPLICANT: Emage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303,569B  
FILING DATE: 07-SEP-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Trujillo, Doreen yako  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CARP-0032  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 943 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 18..722  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 84..722  
US-08-303-569B-4

Query Match  
Best Local Similarity 62.9%; Score 615.6; DB 2; Length 943;  
Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;  
Y 96 CCAGATGTGACATCCAGATGACATCCAGCTCCAGCTCCCTATCTGCATCTGTGGGAGAA 155  
b 76 CCAGAGGACAAATTGTTCTCACCAGCTCTCCAGCAATCATGTCTGCATCTCCAGGGAGA 135  
Y 156 CTGTCCACCATCATGTGCGAGCAAGTGGGAATATTCAAAATTTATTTAGCATGTATCAGC 215  
b 136 AGGTCCACCATGACCTGCAGTGCAGCTCAAGTGT---AGTTACATGAATCGTATCAGC 192  
Y 216 AGACAGAGGAAATCTCTCAGCTCCTGCTATTTCTGCAAAACCTTAGCAGATGGTG 275  
b 193 AGAAGTCAGGACCTCCCTCCCAAGAGATGATTTATGACATCCAACTGGCTTCTGGAG 252  
Y 276 TGCCATCAAGTTTCAGTGCATGTGATCAGGACACAAATATTCTTCAAGATCAACAGCC 335  
b 253 TCCCTGCTCACTTACGGGCGAGTGGGTCTGGGACCTTACTCTCTCAATCAGCGGCA 312  
Y 336 TGCAGCTGAAGATTTGGGAGTTTATCTGTCACATTTTGGAGTACTCGGTACAGT 395  
b 313 TGGAGGCTGAGATGCTGCCACTTATTATCCAGCAGTGGAGTAGTAACCAATTCAGT 372  
Y 396 TCGAGGGGGGACCAAGCTGGAATATAAAACGGCTGTGCTGCACCACTGTATCCATCT 455  
b 373 TCGGCTCGGGGACAAAGTTGGAATATAAACGGGTGTGACTGACCACTGTATCCATCT 432

RESULT 9  
US-08-116-247-4  
Sequence 4, Application US/08116247  
Patent No. 5929212  
GENERAL INFORMATION:  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Zivin, Robert A.  
APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
TITLE OF INVENTION: CD3 Specific Recombinant Antibody  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,247  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/743,377  
FILING DATE: 10-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Paintin, Francis A.  
REGISTRATION NUMBER: 19,386  
REFERENCE/DOCKET NUMBER: CARP-0011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100

us-09-770-916-3.rni

Tue Jul 1 18:41:00 2003

TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 943 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 18..722  
 -08-116-247-4

Query Match 62.9%; Score 615.6; DB 2; Length 943;  
 Best Local Similarity 84.6%; Pred. No. 4.1e-139;  
 Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;

96 CCAGATGTGACATCCAGTACGATGCTCCAGCTCCCTATCTGCTATCTGCTGGGAGAA 155  
 76 CCAGAGGACAAATGTTCTACCCAGCTCCAGCAATCATGCTGCACTCCAGGGGAGA 135  
 156 CTGTCACCATCACATGTCGACAGTGGGAATATTCAAAATATTAGCATGGTATCAGC 215  
 136 AGGTCACCATGACCTGCGAGTCCAGCTCAAGTGT--AAGTTACATGAAGTGTACACG 192  
 216 AGACACAGGAAATCTCCTCAGCTCCTGGTGTATCTGCAAAAACCTTAGCAGATGGT 275  
 193 AGAAGTCAGGACCTCCCCCAAGATGATTTATGACACATCCAACTGGCTTCTGGAG 252  
 276 TGCCATCAAGTTTCAGTGGCATGATCAGGACACAAATATCTCTCAAGATCAACAGCC 335  
 253 TCCCTGCTCACTCAGGGGAGTGGGTCTGGGACCTTTACTCTCAACATCAGCGGCA 312  
 336 TGAGGCTGAAGATTTGGGAGTTATCTGTCACAACTTTTGGAGTACTCCGTACACGT 395  
 313 TGAGGCTGAAGATGCTGCCACTTATCTGCCAGCTGGAGTGGAGTAGTACCCATTCACGT 372  
 396 TCGGAGGGGGACCAAGCTGGAATATAAAGCGGCTGATGTCACCACTGTATCATCT 455  
 373 TCGGCTCGGGGACAAAGTTGGAATATAAAGCGGCTGATGTCACCACTGTATCATCT 432  
 456 TCCACACATCAGTGGAGCTTAACATCTGGAGGTGCTCAGTCGTGCTTCTGAACA 515  
 433 TCCACACATCAGTGGAGCTTAACATCTGGAGGTGCTCAGTCGTGCTTCTGAACA 492  
 516 ACTTCTACCCCAAGACATCAATGTCAGTGAAGATTGATGGAGTGAACGACAAATG 575  
 493 ACTTCTACCCCAAGACATCAATGTCAGTGAAGATTGATGGAGTGAACGACAAATG 552  
 576 GCGTCTGAACAGTTGAGTATCAGGACGCAAGACAGCAGCTACAGCATGAGCAGCA 635  
 553 GCGTCTGAACAGTTGAGTATCAGGACGCAAGACAGCAGCTACAGCATGAGCAGCA 612  
 636 CCCTCAGCTTGACCAAGGACGATGATGACACATACAGCATATACCTGTGAGGCCACTC 695  
 613 CCCTCAGCTTGACCAAGGACGATGATGACACATACAGCATATACCTGTGAGGCCACTC 672  
 696 ACAAGACATCAACTTACCCATTTGCAAGAGCTTCAACAGAAAGTGTAGAGACAAA 755  
 673 ACAAGACATCAACTTACCCATTTGCAAGAGCTTCAACAGAAAGTGTAGAGACAAA 732  
 756 GGTCTGAGACGCCACACAGCTCCAGCTCCATCTATCTCCCTCTCAAGTCTGTG 815  
 733 GGTCTGAGACGCCACACAGCTCCAGCTCCATCTATCTCCCTCTCAAGTCTGTG 791  
 816 GAGGCTTCCCAACAGCGGCTTACCACTGCTGGGTGCTTCCAAACCTCTCCACCTCC 875  
 792 GAGGCTTCCCAACAGCGGCTTACCACTGCTGGGTGCTTCCAAACCTCTCCACCTCC 849  
 876 TTCT 935  
 850 TTCT 909  
 936 TAAAGTGAGTCTTTTGCACAAAACAAAAA 969

Db 910 TAAAGTGAGTCTTTTGCCTTGAACAAAAA 943

RESULT 10  
 US-08-792-824-5  
 ; Sequence 5, Application US/08792824  
 ; Patent No. 5932449  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EMANUEL, PETER A.  
 ; APPLICANT: BURANS, JAMES P.  
 ; APPLICANT: VALDES, JAMES J.  
 ; APPLICANT: MOHYEE, ELDEFRAWI E.  
 ; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: U.S. Army Chemical and Biological Defense  
 ; ADDRESSEE: Command  
 ; STREET: Office of the Chief Counsel, Bldg E4435  
 ; CITY: Aberdeen Proving Ground  
 ; STATE: MD  
 ; COUNTRY: U.S.  
 ; ZIP: 21010-5423  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/792,824  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Biffoni, U. J.  
 ; REGISTRATION NUMBER: 39,908  
 ; REFERENCE/DOCKET NUMBER: DAM 431-96  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 410-671-1158  
 ; TELEFAX: 410-671-2534  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1641 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: CDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mus musculus  
 ; STRAIN: BALB/c  
 ; IMMEDIATE SOURCE:  
 ; CLONE: phist 1  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 87..788 /product= "antibody fragment, light  
 ; OTHER INFORMATION: "chain"  
 ; OTHER INFORMATION: /label= Botfab 1  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 815..1579  
 ; OTHER INFORMATION: /product= "antibody fragment, Heavy  
 ; OTHER INFORMATION: "chain"  
 ; OTHER INFORMATION: /label= Botfab 1  
 ; US-08-792-824-5

Query Match 61.0%; Score 597.2; DB 2; Length 1641;  
 Best Local Similarity 92.2%; Pred. No. 1.3e-134;  
 Matches 651; Conservative 0; Mismatches 53; Indels 2; Gaps 2;  
 51 TGCTCACTCAGGTCCCTGGCTTCTGCTGCTGGCTTACAGGTGCGCATCC 110  
 936 TAAAGTGAGTCTTTTGCACAAAACAAAAA 969

Db 100 TGCTACGGGGCGCTGGATTGTTATTACTCGCTGCCAACAGGCATGGCGACATCC 159  
 QY 111 AGATGACTCAGTCTCAGGCTCCCTATCTGTCATCTGTGGAGAAAGTGTCAACATCATAT 170  
 Db 160 AGATGACCCAGTCTCCAGGCTCCCTATCTGTCATCTGTGGAGAAAGTGTCAACATCATAT 219  
 QY 171 GTCGAGCAAGTGGGATATTTTCAAAATTTATTTAGCATGTTATGAGCAACAGGGAAT 230  
 Db 220 GTCGAGCAAGTGGGATATTTTCAAAATTTATTTAGCATGTTATGAGCAACAGGGAAT 279  
 QY 231 CTCCTCAGTCTCCTGCTGCTATTTGCAAAACCTTAGCAGATGGTGTGCCATCAAGTTCA 290  
 Db 280 CTCCTCAGTCTCCTGCTGCTATATGCAAAACCTTAGCAGATGGTGTGCCATCAAGTTCA 339  
 QY 291 GTGGCAGTGGATCAGGAAACAAATTTCTCAAGATCAACAGCCTGAGGATTT 350  
 Db 340 GTGGCAGTGGATCAGGAAACAAATTTCTCAAGATCAACAGCCTGAGGATTT 399  
 QY 351 TTGGGAGTTTACTGTCAACATTTTGGAGTACTCCGTACAGCTTCCACCATCCAGTG 410  
 Db 400 TTGGGAGTTTACTGTCAACATTTTGGAGTACTCCGTACAGCTTCCACCATCCAGTG 459  
 QY 411 AGCTGGAATTAACAGGCTGATGCTGCACCACTGTATCCATCTTCCACCATCCAGTG 470  
 Db 460 AGCTGGAATTAACAGGCTGATGCTGCACCACTGTATCCATCTTCCACCATCCAGTG 519  
 QY 471 AGCAGTTAATCCTGGAGGCTCAGTCTGCTGCTGCTTGAACAACTTCTACCCCAAAG 530  
 Db 520 AGCAGTTAATCCTGGAGGCTCAGTCTGCTGCTGCTTGAACAACTTCTACCCCAAAG 579  
 QY 531 ACATCAATGTCAGTGGAGGCTGATGCTGCACCACTGTATCCATCTTCCACCATCCAGTG 590  
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 QY 591 GACTGATCAGGACAAAGACAGCAGCCTACAGCATGAGCAGCAGCAGCAGCAGCAGCAGT 650  
 Db 640 GACTGATCAGGACAAAGACAGCAGCCTACAGCATGAGCAGCAGCAGCAGCAGCAGT 699  
 QY 651 AGGACGATGATCAACATACAGTATACCTGTGAGGCTCCTCAAGACAGT 710  
 Db 700 AGGACGATGATCAACATACAGTATACCTGTGAGGCTCCTCAAGACAGT 759  
 QY 711 CACCATTTGTCAGAGCTTCAACAGGATGAGTGTAGACAAAG 756  
 Db 760 C-CCATTTGTCAGAGCTTCAACAGGATGAGTGTAGACAAAG 803

RESULT 11

JS-08-634-783A-2  
 : Sequence 2, Application US/08634783A  
 : Patent No. 5861276  
 : GENERAL INFORMATION:  
 : APPLICANT: KWAK, JU-WON  
 : APPLICANT: HAN, MOON-HI  
 : APPLICANT: CHOL, BYUNG-KWON  
 : TITLE OF INVENTION: C-DNAS ENCODING MURINE ANTIBODY  
 : TITLE OF INVENTION: AGAINST HUMAN PLASMA APOLOPROTEIN B-100  
 : NUMBER OF SEQUENCES: 8  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: DILWORTH & BARRESE  
 : STREET: 333 EARLE OVERTON BLVD.  
 : CITY: UNIONDALE  
 : STATE: NY  
 : COUNTRY: USA  
 : ZIP: 11553  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/634,783A  
 : FILING DATE: 19-APR-1996

CLASSIFICATION: 536  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: BARRESE, ROCCO S.  
 : REGISTRATION NUMBER: 25,253  
 : REFERENCE/DOCKET NUMBER: 685-5  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 516-228-8484  
 : TELEFAX: 516-228-8516  
 : INFORMATION FOR SEQ ID NO: 2:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 642 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : US-08-634-783A-2

Query Match 52.8%; Score 517.2; DB 2; Length 642;  
 Best Local Similarity 87.9%; Pred. No. 1.6e-115;  
 Matches 564; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
 QY 104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGTCATCTGTGGAGAAAGTGTCAAC 163  
 Db 1 GATATCAAGATGACCCAGTCTCCATCTCCATGTATGTCATCTCTAGGAGAGAGAGTCACT 60  
 QY 164 ATCATATGTCGAGCAAGTGGGAATTTTCAAAATTTATTTAGCATGTTATGAGCAACAG 223  
 Db 61 ATCACTTTCAGGAGGAGTCAAGCAATTTATAGCTATTTTAAAGCTGGTTCACAGCAAAACA 120  
 QY 224 GGAATATCTCTCAGTCTGCTGCTATTTCTGCAAAACCTTAGCAGATGTTGTCGATGGG 283  
 Db 121 GGAATATCTCTCAGTCTGCTGCTATTTCTGCAAAACAGATGTTGTCGATGGG 180  
 QY 284 AGTTTCAAGTGGAGTATTTACTGTCACAACTTTTGGAGTACTCCGTACAGTTCGGAGGG 343  
 Db 181 AGTTTCAAGTGGAGTATTTACTGTCACAACTTTTGGAGTACTCCGTACAGTTCGGAGGG 403  
 QY 344 GAAGATTTTGGGAGTATTTACTGTCACAACTTTTGGAGTACTCCGTACAGTTCGGAGGG 463  
 Db 241 GAAGATTTTGGGAGTATTTACTGTCACAACTTTTGGAGTACTCCGTACAGTTCGGAGGG 300  
 QY 404 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCA 463  
 Db 301 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCA 360  
 QY 464 TCCAGTGACAGTTAATCTGAGTGGAGTGGCTCAGTGGTGGTCTTCTTGAACAACTTCTAC 523  
 Db 361 TCCAGTGACAGTTAATCTGAGTGGAGTGGCTCAGTGGTGGTCTTCTTGAACAACTTCTAC 420  
 QY 524 CCAAGAGACATCAATGTCAGTGGAGATTTGATGGCAGTGAACAGCAAAATGGCGTCTG 583  
 Db 421 CCAAGAGACATCAATGTCAGTGGAGATTTGATGGCAGTGAACAGCAAAATGGCGTCTG 480  
 QY 584 AACAGTGGAGTATGATCAGCAGCAACAGCAGCCTACAGCATGAGCAGCAGCAGCAGCAG 643  
 Db 481 AACAGTGGAGTATGATCAGCAGCAACAGCAGCCTACAGCATGAGCAGCAGCAGCAGCAG 540  
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 QY 704 TCAACTTCCACCATTTGCAAGAGCTTCAACAGGATGAGTGT 745  
 Db 601 TCAACTTCCACCATTTGCAAGAGCTTCAACAGGATGAGTGT 642

RESULT 12

US-09-070-817-2  
 : Sequence 2, Application US/09070817  
 : Patent No. 6096516  
 : GENERAL INFORMATION:  
 : APPLICANT: KWAK, JU-WON  
 : APPLICANT: HAN, MOON-HI



Db 121 GGAATATCTCTAAGCCCTGATCTATCTATCAAAAGGATTTGGTAGTGGGTCCCATCA 180  
QY 284 AGTTTCAGTGGCAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCTGCAGCCT 343  
Db 181 AGTTTCAGTGGCAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCTGCAGCCT 246  
QY 344 GAAGATTTGGGAGTTATTTACTGTCAACATTTTGGAGTACTCCGTACAGTTCGAGGG 403  
Db 241 GAAGATTTGGGAGTTATTTACTGTCAACATTTTGGAGTACTCCGTACAGTTCGAGGG 306  
QY 404 GGGACCAAGCTGGAATATAAAGCGGCTGATGCTGACCAACTGTATCCATCTTCCACCA 463  
Db 301 GGGACCAAGCTGGAATATAAAGCGGCTGATGCTGACCAACTGTATCCATCTTCCACCA 366  
QY 464 TCCAGTGGAGCTTTAAACATCTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 523  
Db 361 TCCAGTGGAGCTTTAAACATCTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 426  
QY 524 CCCAAAGACATCAATGTCAAGTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 583  
Db 421 CCCAAAGACATCAATGTCAAGTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 480  
QY 584 AACAGTGGAGCTGATCAGGACAGCAAGACAGCACTACAGCATGAGCAGCACCCTCAG 643  
Db 481 AACAGTGGAGCTGATCAGGACAGCAAGACAGCACTACAGCATGAGCAGCACCCTCAG 540  
QY 644 TTGACCAAGACAGCTGATGAGCAAGATTAAGCACTATACCTGTGAGGCACTTCAAGACA 703  
Db 541 TTGACCAAGACAGCTGATGAGCAAGATTAAGCACTATACCTGTGAGGCACTTCAAGACA 600  
QY 704 TCAACTTCAACCATTTGTCAGAGCTTCAACAGGAATGAGTGTTA 747  
Db 601 TCAACTTCAACCATTTGTCAGAGCTTCAACAGGAATGAGTGTTA 644

## RESULT 14

5453363-1

; Patent No. 5453363

; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF

; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR

; ING AFTER GENETIC EXPRESSION IN PROKARYOTES

; NUMBER OF SEQUENCES: 4

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/206,044

; FILING DATE: 02-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 942,370

; FILING DATE: 09-SEP-1992

; APPLICATION NUMBER: 498,500

; FILING DATE: 23-MAR-1990

; APPLICATION NUMBER: 76,207

; FILING DATE: 23-OCT-1986

SEQ ID NO.1:

LENGTH: 5238

5453363-1

Query Match 49.68; Score 485.8; DB 6; Length 5238;  
Best Local Similarity 82.68; Pred. No. 1e-107;  
Matches 556; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Y 104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTCAAC 163  
b 7 GATATTGTCTACTCAGTCTCCAGCACCCTGTCTGTGACTCCAAGAGATAGCGTCAGT 66

Y 164 ATCAGATGTCAGCAAGTGGGAATATCAAAATTTATAGCATGGTATCAGCAGACAG 223  
b 67 CTTCCTGCGAGCGCCAGCAAGTATTAGCAACACTACATGGTATCAACAAAATCA 126

Y 224 GGAATATCTCCTCAGTCTCTGGTCTATTCTGCAAAAACCTTAGCAGATGCTGTCATCA 283  
b 127 CATGAGTCTCCAAGGCTTCTCATCAATATGCTTCCAGTCCATCTCTGGGATCCCTCT 186

QY 284 AGTTTCAGTGGCAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCTGCAGCCT 343  
Db 187 AGTTTCAGTGGCAGTGGATCAGGACACAAATATCTCTCAAGATCAACAGCCTGCAGCCT 246  
QY 344 GAAGATTTGGGAGTTATTTACTGTCAACATTTTGGAGTACTCCGTACAGTTCGAGGG 403  
Db 247 GAAGATTTGGGAGTTATTTACTGTCAACATTTTGGAGTACTCCGTACAGTTCGAGGG 306  
QY 404 GGGACCAAGCTGGAATATAAAGCGGCTGATGCTGACCAACTGTATCCATCTTCCACCA 463  
Db 307 GGGACCAAGCTGGAATATAAAGCGGCTGATGCTGACCAACTGTATCCATCTTCCACCA 366  
QY 464 TCCAGTGGAGCTTTAAACATCTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 523  
Db 367 TCCAGTGGAGCTTTAAACATCTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 426  
QY 524 CCCAAAGACATCAATGTCAAGTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 583  
Db 427 CCCAAAGACATCAATGTCAAGTGGAGTGCCTCAGTCGTCGTCTTCTTGAACAACTTCTAC 486  
QY 584 AACAGTGGAGCTGATCAGGACAGCAAGACAGCACTACAGCATGAGCAGCACCCTCAG 643  
Db 487 AACAGTGGAGCTGATCAGGACAGCAAGACAGCACTACAGCATGAGCAGCACCCTCAG 546  
QY 644 TTGACCAAGACAGCTGATGAGCAAGATTAAGCACTATACCTGTGAGGCACTTCAAGACA 703  
Db 547 TTGACCAAGACAGCTGATGAGCAAGATTAAGCACTATACCTGTGAGGCACTTCAAGACA 606  
QY 704 TCAACTTCAACCATTTGTCAGAGCTTCAACAGGAATGAGTGTTA 763  
Db 607 TCAACTTCAACCATTTGTCAGAGCTTCAACAGGAATGAGTGTTA 666  
QY 764 GACGCCACCAACCA 776  
Db 667 GACGCCACCAACCA 679

## RESULT 15

US-09-170-769A-7

; Sequence 7, Application US/09170769A

; Patent No. 6444206

; GENERAL INFORMATION:

; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE

; APPLICANT: LETURCO, Didier

; APPLICANT: MORIATRY, Ann

; APPLICANT: ULEVITCH, Richard

; APPLICANT: TOBIAS, Peter

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT

; FILE REFERENCE: SCRIPT1140-3

; CURRENT APPLICATION NUMBER: US/09/170,769A

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: US 08/070,160

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 633

; TYPE: DNA

; ORGANISM: Murine

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(633)

; OTHER INFORMATION: CDR1-Nucleic acids 61-93; CDR2-Nucleic acids 139-159; CDR3-Nuc

; OTHER INFORMATION: c acids 256-28

US-09-170-769A-7

Query Match

Best Local Similarity 49.38; Score 482.6; DB 4; Length 633;

Matches 539; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 113 ATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTCAACATGT 172

Db 1 ATGACCCAGACTCCATCTCCCTCTCTGCTCTCTGAGGAGACAGAGTCAACATCAGTTGC 60

us-09-770-916-3.rni

Search completed: June 24, 2003, 01:22:35  
Job time : 55.8675 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:23:42 ; Search time 245.227 Seconds  
(without alignments)  
8990.482 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 accaccttctgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	ID	Description
1	708.6	72.4	751	16	AAT51437
2	693.4	70.8	1041	15	Murine MAB SK48-E2
3	693.4	70.8	1041	15	T84.12 light chain
4	677	69.2	882	5	AA054653
5	673.8	68.8	882	5	T84.12 L4-12-1 lig
6	667.6	68.2	927	20	cDNA insert of pK1
7	652	66.6	961	16	mRNA encoding kapp
8	650.6	66.5	952	16	Anti-p21(ras) mono
9	634.2	64.8	5711	24	Anti-tobacco mosai
					MAB 55.1 light cha
					Alpha-lactalbumin

10	634.2	64.8	6255	24	AAD28276	LNBDTC vector #1.
11	634.2	64.8	6255	24	AAD28315	LNBDTC vector #1.
12	634.2	64.8	7170	24	AAD28272	LSRNL vector. Chi
13	626	63.9	1644	20	AA86667	Murine anti-botuli
14	626	63.9	1672	20	AA86664	Murine anti-botuli
15	626	63.9	4435	20	AA86663	Murine anti-botuli
16	622.8	63.6	1632	20	AA86666	Murine anti-botuli
17	615.6	62.9	943	12	AAQ12636	Monoclonal antibod
18	598	61.1	882	14	AAQ48038	Monoclonal antibod
19	597.2	61.0	1641	20	AA86665	Murine anti-botuli
20	535	54.6	831	24	AA86665	Human penton base
21	517.2	52.8	642	18	AA86665	Mouse monoclonal a
22	509.6	52.1	652	17	AA86665	Antibody 3G2 light
23	485.8	49.6	5238	11	AAQ04654	Plasmid pBT11 enc
24	483.2	49.4	724	20	AAQ04654	Chimeric antibody
25	476	48.6	1106	24	AAQ04654	Human ovarian anti
26	464.2	47.4	645	21	ABK1286	Mouse agglutinatio
27	461.4	47.1	705	24	AA86665	DNA encoding TRA-8
28	460.2	47.0	1066	14	AA86665	Human anti-HBs lig
29	459.2	46.9	714	20	AAQ49943	Mouse immunoglobul
30	459	46.9	944	22	AAQ49943	Human breast cance
31	458.8	46.9	723	16	AAQ49943	Human antibody F4-
32	455.4	46.5	627	16	AAQ49943	Monoclonal antibod
33	453.8	46.4	678	21	AAQ49943	WOW-1 Fab light ch
34	453.2	46.3	974	24	AA86665	Anti-human AILIM m
35	452.2	46.2	738	10	AA86665	Chimeric antibody
36	452	46.2	738	21	AA261037	Nucleotide sequenc
37	450.4	46.0	1735	22	AAH47858	Mouse 6D9 catalyti
38	449.4	45.9	732	17	AAH47858	Murine A5B57 Light
39	449.4	45.9	732	17	AAH47858	Plasmid pE14/A5B7
40	447.8	45.7	717	18	AAH47858	L chain subunit of
41	447.8	45.7	717	19	AAH47858	Anti-human Fas mon
42	447.8	45.7	717	21	AAH47858	Anti-human Fas ant
43	447.8	45.7	1526	13	AAQ21097	FabD1.3 in pUC19.
44	446.6	45.6	714	19	AAV70130	Anti-Fas MAB HFE7A
45	446.6	45.6	714	21	AAA72109	CDNA encoding mous

ALIGNMENTS

RESULT 1  
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ID AAT51437 standard; DNA; 751 BP.  
XX AAT51437;  
AC AAT51437;  
XX  
DT 24-JUN-1997 (first entry)  
DE Murine MAB SK48-E26 light chain DNA.  
XX  
KW Interleukin-1 beta; IL-1 beta; recombinant antibody;  
KW humanised antibody; chimeric antibody; antibody engineering;  
KW monoclonal antibody; MAB; SK48-E26; inflammation; therapy; ds.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT FT /\*tag= a  
FT FT /note= "cloning adaptor"  
FT FT 15..32  
FT FT /\*tag= b  
FT FT 33..737  
FT FT /\*tag= c  
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FT FT 738..751  
FT FT /\*tag= f  
FT FT /note= "cloning adaptor"



[illegible]

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Q54653  
AAQ5  
AAQ5  
24-J

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DE	
XX	
KW	Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;
KW	region; transform; myeloma cell; light chain; tumour; ss.
XX	Synthetic.
OS	
XX	
FH	Location/Qualifiers
FT	CDS 34..950
FT	/*tag= a
FT	/product= T84.12_L4-12-1_light_chain
XX	
PN	WO9325237-A.
XX	
PD	23-DEC-1993.
XX	
PF	15-JUN-1993; 93WO-US05709.
XX	
PR	15-JUN-1992; 92US-0904074.
XX	
PA	(CITY ) CITY OF HOPE.
PA	(YANG/) YANG Y.
XX	
PI	Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;
PI	Yang YH;
XX	
DR	WPI; 1994-007204/01.
DR	P-PSDB; AAR47451.
XX	
PT	New chimaeric T84.12 antibody active against carcinoembryonic
PT	antigen - has murine variable and human constant regions, also
PT	DNA encoding it and transformed myeloma cells
XX	
PS	Claim 1; Page 19; 27pp; English.
XX	
CC	The sequences (AAQ54651-52) show the light and heavy chain cDNAs
CC	of murine T84.12. The T84.12 antibody is directed against the
CC	tumour marker carcinoma embryonic antigen, and is useful for
CC	tumour imaging and immunotherapy.
XX	
SQ	Sequence 1041 BP; 322 A; 266 C; 213 G; 240 T; 0 other;
	Query Match 70.8%; Score 693.4; DB 15; Length 1041;
	Best Local Similarity 85.0%; Pred. NO. 8.8e-132;
	Matches 788; Conservative 0; Mismatches 136; Indels 3; Gaps 1;
QY	56 ACTCAGGTCTCGCGTGGCTGCTGCTGCTGCATCTGTGGGAGAACTGTGCCATCACATGTCGA 175
Db	
	46 ACTCAGGTCTTTGTATACATGTTGCTSTGTTGCTCTGGTGTTGATGGAGACAATTGTGCTG 105
QY	116 ACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTGCCATCACATGTCGA 175
Db	
	106 ACCCAGTCTCAAATAATTCATGTCACATCAGTTGGAGGCACGGTCACCTGCAAG 165
QY	176 GCAAGTGGGAATATTCAAAATTTATTTAGCATGGTATCAGCAGACACAGGGAAAAATCTCCT 235
Db	
	166 GCCAGTCAAAATGTCATFACATAATGTTGCCCTGGTATCAACAGAAACCAGGACAATCTCCT 225
QY	236 CAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGTTTCAGTGGC 295
Db	
	226 AAAGCACTGATTTACTCGGCATCTACCGTTACAGTGGAGTCCCTGTATCGCTTCACAGC 285
QY	296 AGTGATCAGGAACACAATAATCTCTCAAGATCAACAGCCTGCGAGCTGAAGATTTTGGG 355
Db	
	286 AGTGATCTGGACAGAGATTTCACCTCTCACCATCAGCAATGTGCAGTCTGAAGACTTGGCA 345
QY	356 AGTTATTACTGTCAACATTTTGGAG---TACTCCGTACAGTTTCGGAGGGGGGACCAAG 412
Db	
	346 GAATATTCTGTACGAATGTAAACAGGTATCCTCTATTACGTTTCGGCTCGGGGACAACG 405
QY	413 CTGGAATAAACCGGCTGATCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGA 472

Tue Jul 1 18:40:59 2003

406 TTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTCCACCATCCAGTGAG 465  
 473 CAGTTAATCTCTGGAGTGGCTCAGTCTGCTGCTTCTTGAACAACTTCTACCCCAAGAC 532  
 466 CAGTTAATCTCTGGAGTGGCTCAGTCTGCTGCTTCTTGAACAACTTCTACCCCAAGAC 525  
 533 ATCAATCTCAAGTGAAGATTTGATGGCAGTGAACGACAAATGCGCTCTGAAACAGTTGG 592  
 526 ATCAATCTCAAGTGAAGATTTGATGGCAGTGAACGACAAATGCGCTCTGAAACAGTTGG 585  
 593 ACTGATCAGGACAGCAAGACAGACACCTACAGCATGAGCAGCACCCTCAGCTTGACCAAG 652  
 586 ACTGATCAGGACAGCAAGACAGACACCTACAGCATGAGCAGCACCCTCAGCTTGACCAAG 645  
 653 GACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCA 712  
 646 GACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCA 705  
 713 CCCATTTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGTCTCTGAGACGCCACC 772  
 706 CCCATTTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGTCTCTGAGACGCCACC 765  
 773 ACCAGCTCCCGAGCTCCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 832  
 766 ACCAGCTCCCGAGCTCCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 825  
 833 GACCTACCACTCTTGGGCTGCTTCCAAACCTCTCTCCACCTCTCTCTCTCTCTCTCTCTCT 892  
 826 GACCTACCACTCTTGGGCTGCTTCCAAACCTCTCTCCACCTCTCTCTCTCTCTCTCTCTCT 885  
 893 TTCCTTGGCTTTTATCATGCTAATATTTCCGAGAAATATTTCAATTAAGTGAAGTCTTTGCA 952  
 886 TTCCTTGGCTTTTATCATGCTAATATTTCCGAGAAATATTTCAATTAAGTGAAGTCTTTGCA 945  
 953 AAAAAAAAAAAAAAAAAAAAAAAAAA 979  
 946 CTTGAAAAAAAAAAAAAAAAAAAAA 972

RESULT 4

AN40022

AN40022 standard; cDNA; 882 BP.

AN40022;

01-DEC-1991 (first entry)

cDNA insert of pk17G4 encoding kappa anti-carcinoembryonic antigen.

Immunoglobulin; ds DNA; carcinoembryonic antigen; vector pk17G4.

EPI25023-A.

14-NOV-1984.

06-APR-1984; 84EP-0302368.

08-APR-1983; 83US-0483457.

(CITY ) CITY OF HOPE.

(GETH ) GENENTECH INC.

Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;

WPI; 1984-283749/46.

Immunoglobulin(s) produced by recombinant host cells - useful as

antibodies analogous to forms from mammals.

Disclosure; Fig. 2A-B; 79pp; English.

The cDNA is contained within recombinant vector pk17G4 and encodes

kappa anti-carcinoembryonic antigen chain. Using the vector the

CC immunoglobulin is produced readily in pure monoclonal form. Genetic  
 CC manipulations can be used to produce chimeras of variants drawing  
 CC their homology from species differing from each other. Protein  
 CC manipulation is also possible.

xx Sequence 882 BP; 231 A; 243 C; 194 G; 214 T; 0 other;

Query Match 69.2%; Score 677; DB 5; Length 882;  
 Best Local Similarity 85.7%; Pred. No. 1.9e-128;  
 Matches 752; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 76 GCTGCTGTGGCTTACAGTGCCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCT 135  
 Db 1 GTTCTGTGGTGTCTGCTGTTGAAGAGAGATTTGTGATGACCCAGTCTCAAAATTCAT 60  
 QY 136 ATCTGATCTGTGGGAGAACTGTCAACATCACATGTGAGCAAGTGGGAATATTCAAAA 195  
 Db 61 GTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGGTGC 120  
 QY 196 TTATTTAGATGGTATCAGCAGACAGGAAATCTCTCAGCTCTGGTCTATTCTGTC 255  
 Db 121 TGTATAGCTGTGATCAACAGAAACAGGAGCAATCTCTAACTACTGATTTACTGGSC 180  
 QY 256 AAAAACCTTAGCAGATGTGTGCCATCAAGTTCAGTGGCAGTGGATCAGGAACAATA 315  
 Db 181 ATCCACCCGGGACACTGGAGTCCCTGATCGCTTCACAGCAGTGGATCTGGACAGATT 240  
 QY 316 TTCTCTCAAGATCAACAGCCTGCAGCTGAAGATTTGGAGTATTACTGTCAACATT 375  
 Db 241 CACTCTCAACATTAACAAATGTGAGTCTGATGACTTGGCAGATTTATTTGTCAACAATA 300  
 QY 376 TTGGAGTACTCCGTACACGTTTCGGAGGGGGACCAAGCTTGGAAATAAAGGGCTGATGC 435  
 Db 301 TAGGGGTATCTCTCACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAACGGGCTGATGC 360  
 QY 436 TGCACCACTGTATCCATCTTCCACCATCTCCAGTGCAGTGAAGTAACTCTGGAGTGCCTC 495  
 Db 361 TGCACCACTGTATCCATCTTCCACCATCTCCAGTGCAGTGAAGTAACTCTGGAGTGCCTC 420  
 QY 496 AGTCGTGTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGAAGATTGA 555  
 Db 421 AGTCGTGTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGAAGATTGA 480  
 QY 556 TGGCAGTGAACGACAAATGGCGTCTGAAACAGTGGACTGATCAGGACAGCAAGACAG 615  
 Db 481 TGGCAGTGAACGACAAATGGCGTCTGAAACAGTGGACTGATCAGGACAGCAAGACAG 540  
 QY 616 CACCTACAGCATGAGCAGCACCCTCAGTTTACCAAGGAGGATGATGAACGACATAACAG 675  
 Db 541 CACCTACAGCATGAGCAGCACCCTCAGTTTACCAAGGAGGATGATGAACGACATAACAG 600  
 QY 676 CTATACCTGTGAGGCCACTCACAAGACATCAACTTCAACCCATTGTCAAGAGCTTTCAACAG 735  
 Db 601 CTATACCTGTGAGGCCACTCACAAGACATCAACTTCAACCCATTGTCAAGAGCTTTCAACAG 660  
 QY 736 GAATCAGTGTGAGACAAAGTCTGAGAGCGCCACCAAGGAGTCCACAGCTCCCAAGCTCCTA 795  
 Db 661 GAATCAGTGTGAGACAAAGTCTGAGAGCGCCACCAAGGAGTCCACAGCTCCCAAGCTCCTA 720  
 QY 796 TCTTCCCTTCTAAGGTCTTGGAGGCTTCCCAAGGAGGAGTCCCAAGGAGTCCCAAGGAGTCC 855  
 Db 721 TCTTCCCTTCTAAGGTCTTGGAGGCTTCCCAAGGAGGAGTCCCAAGGAGTCCCAAGGAGTCC 780  
 QY 856 CAAACCTCTCCCAAGGAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 915  
 Db 781 CAAACCTCTCCCAAGGAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840  
 QY 916 TATTTGAGAAATATTTCAATAAAGTGAAGTCTTTGCA 952  
 Db 841 TATTTGAGAAATATTTCAATAAAGTGAAGTCTTTGCA 877

RESULT 5

AAAN40023	
ID	AAAN40023 standard; mRNA; 882 BP.
XX	AAAN40023;
XX	
DT	01-DEC-1991 (first entry)
DE	mRNA encoding kappa anti-carcinoembryonic antigen.
XX	
KW	Immunoglobulin; ss mRNA; carcinoembryonic antigen.
XX	
FH	Key
FT	1..673
FT	/*tag= a
XX	
PN	EP125023-A.
XX	
XX	14-NOV-1984.
XX	
PF	06-APR-1984; 84EP-0302368.
XX	
XX	08-APR-1983; 83US-0483457.
XX	
XX	(CITY ) CITY OF HOPE.
XX	(GETH ) GENENTECH INC.
XX	
XX	Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;
XX	
XX	WPI: 1984-283749/46.
XX	P-PSDB; AAP40031.
XX	
XX	Immunoglobulin(s) produced by recombinant host cells - useful as
XX	antibodies analogous to forms from mammals.
XX	
XX	Disclosure; Fig. 3; 79pp; English.
XX	
XX	The mRNA is the coding sequence of the cDNA fragment contained within
XX	recombinant vector pK17G4 (see AAAN40022). It encodes kappa anti-
XX	carcinoembryonic antigen chain. Using the vector the immunoglobulin is
XX	produced readily in pure monoclonal form. Genetic manipulations can be
XX	used to produce chimeras of variants drawing their homology from species
XX	differing from each other. Protein manipulation is also possible.
XX	
XX	Sequence 882 BP; 231 A; 244 C; 194 G; 213 U; 0 other;
XX	
XX	Query Match 68.8%; Score 673.8; DB 5; Length 882;
XX	Best Local Similarity 64.5%; Pred No. 8.3e-128;
XX	Matches 566; Conservative 184; Mismatches 127; Indels 0; Gaps 0;
Y	76 GCTGCTGTGGCTTACAGGTGCCAGATGTGCATCCAGATGACTCAGTCTCCAGCCTCCCT 135
b	:  :
b	1 GUUGCUGUGUGUCUGUGUUGAAGGAGACAUUGUGAUGACCAGUCUCACAAAUCAU 60
Y	136 ATCTGCATCTGTGGGAGAACTGTCCATCATGTGTGCAGCAAGTGGGAATATTCAAA 195
b	:  :
b	61 GUCCACACAGUAGGACAGAGGCGUCAGCAUCCUGCAAGCCAGACGAGUUGGUGC 120
Y	196 TTATTTCATGTTATCAGCAGACACAGGGAAAATCTCTCAGTCTCTGTGTTATTCGC 255
Y	: :  :
b	121 UGUUAGCCUGGUUAACAAGAACACAGGACAAUCCUAAUCUAGAUUUAUCUGGC 180
Y	256 AAAAACCTTTAGCAGATGGTGTGCCATCAAGTTTCAGTGGCAGTGATCAGGAACAATA 315
Y	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b	181 AUCCACCGGCACACUGGAGUCCUUCUAGCUCUAGCAGGAGUUGGGACAGAUU 240
Y	316 TTCTCTCAAGATCAACACGCTGCAGCCTGAAGATTTTGGGAGTATTACTGTCAACATTT 375
Y	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b	241 CACUCUACCAUUGACAUUGCAGUCUGAUGACUUGGGCAGAUUUUUCUGUACAANA 300
Y	376 TTGAGGTACTCCGTACACGTTTCGGAGGGGGACCAAGCTGGAATAAAAGCGCTGATGC 435
Y	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b	301 UAGCGGUAUCCUCUCACGCUUGCUGGACGACCAAGCUGCAGUUAUUUCUGUACAANA 360

[illegible]

## RESULT 6

RESULT 6	
AAAX79347	
ID	AAAX79347 standard; cDNA; 927 BP.
XX	
AC	AAAX79347;
XX	
DT	31-AUG-1999 (first entry)
XX	
DE	Anti-p21(ras) monoclonal antibody Y13-259 light chain gene.
XX	
KW	Inhibition; function; recombinant; p21; ras; monoclonal antibody;
KW	light chain; activity; cancer; neoplasm; oncogene; ds.
XX	
OS	Mus sp.
XX	
PN	US5919650-A.
XX	
PD	06-JUL-1999.
XX	
PF	22-APR-1991; 91US-0690192.
XX	
PR	22-APR-1991; 91US-0690192.
XX	
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Barbacid M, Montano X;
XX	
DR	WPI; 1999-394621/33.
DR	P-PSDB; AAY14557.
XX	
PT	Inhibiting protein function using recombinant, intracellularly
XX	expressed antibodies
PS	Claim 9; Column 15-16; 23pp; English.
XX	
CC	The invention relates to a method for inhibiting protein function



Mus sp.	Key	Location/Qualifiers
XX OS XX	CDS	16..735
XX FH XX		/*tag= a
XX FT XX		16..75
XX FT XX	sig_peptide	/*tag= b
XX FT XX		76..732
XX FT XX	mat_peptide	/*tag= c
XX PN XX		WO9515382-A.
XX PD XX		08-JUN-1995..
XX PF XX		29-NOV-1994; 94WO-GB02610.
XX PR XX		03-JUN-1994; 94GB-0011089.
XX PR XX		03-DEC-1993; 93GB-0024819.
XX PA XX		(ZENE ) ZENECA LTD.
XX PI XX	Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;	
XX PI XX	Rose MS, Wright AF;	
XX DR XX	WPI: 1995-215262/28.	
XX DR XX	P-PSDB; AAR76087.	
XX PT XX	Antigen binding structures containing CDRs recognising the CA55.1	
XX PT XX	antigen - produced by hybridomas and host cells, for use in the	
XX PT XX	diagnosis and therapy of cancer	
XX PS XX	Disclosure; Fig.16; 121pp; English.	
XX CC XX	Mab 55.1 (ECACC 93081901) recognises the colorectal tumor-associated	
XX CC XX	antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)	
XX CC XX	chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or	
XX CC XX	V-min humanized 55.1 constructs have been expressed in myeloma	
XX CC XX	cells and E. coli.	
XX CSQ	Sequence 952 BP; 245 A; 268 C; 215 G; 224 T; 0 other;	
Query Match	56.5%; Score 650.6; DB 16; Length 952;	
Best Local Similarity	83.8%; Pred. No. 4.3e-123;	
Matches	780; Conservative 0; Mismatches 129; Indels 22; Gaps 3;	
39	CAGTCATGAGTGTGCTCACTCAGGTCGTGGCGTTGCTGCTGCTGTGGCTTACAGGTGCCA	98
11	CCGCGATGGATTCAACAGGCCAGGTTCTATATTGCTGCTGCTATGGTATCTGGACCT	70
99	GATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTG	158
71	GTGGGACATTTGTGATGTACAGTCTCCATCCTCCCTGGCTGTGTACAGCAGGAGAAGG	130
159	TCACCATCATGTGCGAGCAGTGGGAATATTC-----AAAAATTATT	200
131	TCACCATGAGTGCRAATCCAGTCAGATCTCTCAACAGTAGAACCCGAAAGAACTACT	190
201	TAGCATGGTATCAGCAGACACAGGGAATAATCTCCTCAGCTCCCTGGTCTATTCTGCAAAA	260
191	TGGCTTGGTATCAGCAGACAGACAGGCGAGTCTCTAACTGCTGATCTATTGGGCAATCA	250
261	CCTTAGCAGATGGTGTGCCATCAAGTTTCACTGGCAGTGGATCAGGAACAATAATCTC	320
251	CPAGGACATCTGGGTCCTGATCGCTTCACAGCAGTGGATCTGGACAGATTTCACTC	310
321	TCAAGATCAACAGCTCGAGCCTCAAAATTTTGGGAGTTATTACTGTCAACATTTTGGGA	380
311	TCACCAUCAGCAGTGTGAGGCTGAAGACCTGGCAATTTATTACTCAAGCAATCTT---	367
381	GTACTCCGTACACCTTCGGAGGGGGACCAAGCTGGAAATTAACACGGCTGATGCTGCAC	440
368	ATACTCTCGGACGTTCCGTTGGAGGACCAGCTGGAAATTAACACGGCTGATGCTGCAC	427

	CDS	2387..2443 /*tag= c /product= "cc49 signal peptide coding region" 2444..3088
	CDS	/*tag= d /product= "Bot antibody light chain Fab coding region" 3112..3686 /*tag= e /note= "EMCV IRES"
	misc_feature	3687..3745 /*tag= f /product= "Bovine alpha-lactalbumin signal peptide coding region" 3746..4443
	CDS	/*tag= g /product= "Bot antibody heavy chain Fab coding region" 4481..5072 /*tag= h /note= "WPRE sequence"
	LTR	5118..5711 /*tag= i /note= "MoMuLV 3' LTR"
	XX	WO200202783-A2.
	PN	10-JAN-2002.
	PD	29-JUN-2001; 2001WO-US20714.
	PX	03-JUL-2000; 2000US-215851P.
	PA	(GALA-) GALA DESIGN INC. Bleck GT;
	PI	WIPO; 2002-154749/20.
	DR	Noel regulatory elements including nucleic acid encoding hybrid alpha-lactalbumin promoter or mutant RNA export element, for expressing one or more proteins e.g. antibodies, pharmaceutical proteins in host cells -
	XX	Example 1; Fig 11; 151pp; English.
	CC	The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further provides methods of indirectly detecting the expression of a protein of interest, comprising providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein operably linked by an internal ribosome entry site (IRES), and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein indicates the presence of desired protein. Regulatory elements and vectors of the invention are useful for the production of immunoglobulin (Ig), preferably secretory Ig. They are useful in the expression of one or more proteins such as erythropoietin, growth hormone, insulin, immunoglobulins, protein C, cytokines and their receptors, hormones, Von Willebrand's factor, lung surfactant, serum albumin, DNase, vascular endothelial growth factor, receptors for hormones or growth factors, rheumatoid factors, nerve growth factors, CD proteins, osteoinductive factors, immunotoxins, bone morphogenetic protein, interferons, colony stimulating factors, surface membrane proteins, superoxide dismutase, T-cell receptors, addressins, regulatory proteins, viral antigens, transport proteins and their fragments. The vectors are particularly useful for expressing G protein coupled receptors and other transmembrane proteins. The retroviral vectors are useful for expressing proteins in mammalian tissue culture host cells, including rat fibroblast cells, bovine kidney cells and human kidney cells. The present vector is alpha lactalbumin (LA) Bot vector used in the invention. The vector comprises the following elements: bovine/human alpha-lactalbumin hybrid promoter, double mutated pre-mRNA processing enhancer (PPE) sequence;
	Key	Location/Qualifiers
	misc_feature	1..2053 /*tag= a /note= "Bovine/human alpha-lactalbumin 5' flanking region"
	misc_feature	2093..2336 /*tag= b



cc49 signal peptide, botulinum toxin antibody light chain, IRES from  
encephalomyocarditis virus (ECMV), Bovine alpha-lactalbumin signal  
peptide, botulinum toxin antibody heavy chain, woodchuck mRNA processing  
enhancer (WPRE) sequence and 3' moloney murine leukemia virus (MoMuLV)  
LTR.  
Sequence 5711 BP; 1408 A; 1424 C; 1434 G; 1445 T; 0 other; .  
SQ

[illegible]

## RESULT 10

AD28276

0 AAD28276 standard; DNA; 6255 BP.

AAD28276;

2

22-APR-2002 (first entry)

1

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

DE	LNBOTDC vector #1.	
XX		
KW	Bovine; alpha-lactalbumin; pharmaceutical; industrial; ECMV; IRES	
KW	encephalomyocarditis virus; diagnostic; internal ribosome entry s	
KW	screening; cytomegalovirus; moloney murine leukemia virus; MoMuLV	
KW	botulinum; ds.	
XX		
OS	Chimeric - Encephalomyocarditis virus.	
OS	Chimeric - Clostridium botulinum.	
OS	Chimeric - Moloney murine leukemia virus.	
OS	Chimeric - Bos sp.	
OS	Chimeric - Cytomegalovirus.	
OS	Chimeric - Unidentified.	
XX		
PH	Key	Location/Qualifiers
FT	LTR	1..589
FT		/*tag= a
FT		/note= "MoMuLV 5' LTR"
FT	misc_feature	559..1468
FT		/*tag= b
FT		/note= "MoMuLV Extended packaging region"
FT	misc_feature	1512..2306
FT		/*tag= c
FT		/note= "Neomycin resistance gene"
FT	promoter	2656..3473
FT		/*tag= d
FT		/note= "CMV promoter"
FT	CDS	3516..3572
FT		/*tag= e
FT		/product= "cc49 signal peptide coding region"
FT	misc_feature	3573..4217
FT		/*tag= f
FT		/note= "Bot Fab 5 light chain"
FT	misc_feature	4235..4816
FT		/*tag= g
FT		/note= "EMCV IRES"
FT	CDS	4817..4873
FT		/*tag= h
FT		/product= "Modified bovine alpha-LA signal peptide coding region"
FT	misc_feature	4874..5572
FT		/*tag= i
FT		/note= "Bot Fab 5 heavy chain"
FT	LTR	5662..6255
FT		/*tag= j
FT		/note= "MoMuLV 3' LTR"
XX		
PN	WO200202738-A2.	
XX*		
PD	10-JAN-2002.	
XX		
PF	29-JUN-2001; 2001WO-US20710.	
XX		
PR	03-JUL-2000; 2000US-215925P.	
XX		
PA	(GALA-) GALA DESIGN INC.	
XX		
PI	Bremel RD, Miller LU, Bleck GT, York D;	
XX		
DR	WPI; 2002-154737/20.	
XX		
PT	Host cell for producing a desired protein and for screening compounds	
PT	useful for pharmaceutical, industrial, diagnostic and other purposes	
PT	comprises multiple integrating vectors having an exogenous gene	
XX		
PS	Example 3; Fig 15; 191pp; English.	
XX		
CC	The invention relates to a host cell comprising a genome having at l	
CC	two integrated integrating vectors. The integrating vectors comprise	
CC	at least one exogenous gene operably linked to a promoter. The host cell	
CC	is useful for producing a desired protein and for comparing protein	
CC	functions. The host cells comprises a reporter gene which is from ge	
CC	fluorescent protein. Lucif.	







CC this invention binds to the non-neurotoxic proteins that are found in  
CC neurotoxin complexes A and B. Such antibody fragments are able to  
CC act as immunosensors for detecting botulinum toxins in food and  
CC are also useful in health care and in military applications. They  
CC are less expensive to produce than monoclonal antibodies as they can be  
CC isolated from large scale bacterial cultures. Also, the affinity of an  
CC rFab may be altered by mutagenesis of its gene and subsequent screening  
CC of the expressed rFabs.  
XX  
SQ

Sequence 1644 BP; 438 A; 446 C; 402 G; 358 T; 0 other;

Query Match 63.9%; Score 626; DB 20; Length 1644;  
Best Local Similarity 92.9%; Pred. No. 4.6e-118;  
Matches 656; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 51 TGCCTCACTCAGTCCCTGGGGTTCTGCTGCTGTACAGGTGCAGATGTGACATCC 110  
DB 101 TGCCTACGGCGCGCTGGATTGTTATTACTGCTGCCCAACAGCCATGGCGGACATCC 160  
QY 111 AGATGACTCAGTCTCAGGCTCCCTATCTGCTGTGGGAAACTGTACCATCACAT 170  
DB 161 AGATGACCCAGTCTCAGGCTCCCTATCTGCTGTGGGAAACTGTACCATCACAT 220  
QY 171 GTCGAGCAAGTGGGAATATTCAAAATATTAGTATGATGATCAGCAGACAGGAAAT 230  
DB 221 GTCGAGCAAGTGGGAATATTCAAAATATTAGTATGATGATCAGCAGACAGGAAAT 280  
QY 231 CTCTCAGCTCTGCTCTATTCTGCAAAACCTTAGCAGATGCTGCTGATCAGATTC 290  
DB 281 CTCTCAGCTCTGCTCTATTATGCAAAACCTTAGCAGATGCTGCTGATCAGATTC 340  
QY 291 GTGGCAGTGGATCAGGAACAATATTCTCAAGATCAACAGCTGCTGAGCTGAAGATT 350  
DB 341 GTGGCAGTGGATCAGGAACAATATTCTCAAGATCAACAGCTGCTGAGCTGAAGATT 400  
QY 351 TTGGGAGTTATTCTGCAACATTTTGGAGTACTCCGTACAGCTTCCGGGGGGACCA 410  
DB 401 TTGGGAGTTATTCTGCAACATTTTGGAGTACTCCGTGAGCTTCCGGGGGGACCA 460  
QY 411 AGCTGGAATTAACACGGCTGATGCTGCAACATTTTGGAGTACTCCGTGAGCTTCC 470  
DB 461 AGCTGGAATTAACACGGCTGATGCTGCAACATTTTGGAGTACTCCGTGAGCTTCC 520  
QY 471 AGCAGTTAATCATCTGGAGTGCCTCAGTCTGCTGCTTCTTGAACAACTTACCCCA 530  
DB 521 AGCAGTTAATCATCTGGAGTGCCTCAGTCTGCTGCTTCTTGAACAACTTACCCCA 580  
QY 531 ACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAATATGCTGCTGAGCA 590  
DB 581 ACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAATATGCTGCTGAGCA 640  
QY 591 GGACTGATCAGGACAGAAAGACAGCACCCTACAGCATGAGCAGCACCCTCAGCTG 650  
DB 641 GGACTGATCAGGACAGAAAGACAGCACCCTACAGCATGAGCAGCACCCTCAGCTG 700  
QY 651 AGGACGAGTATGACACACATACAGATATACCTGTGAGGCTACACAGACATCAACT 710  
DB 701 AGGACGAGTATGACACACATACAGATATACCTGTGAGGCTACACAGACATCAACT 760  
QY 711 CACCCATTGTCAGAGCTTCAACAGAAATGAGTGTAGACAAAG 736  
DB 761 CACCCATTGTCAGAGCTTCAACAGAAATGAGTGTAGACAAAG 806

RESULT 14

AX86664

AX86664 standard; cDNA; 1672 BP.

AX86664;

20-OCT-1999 (first entry)

Murine anti-botulinum toxin antibody fragment (BotFab 5) cDNA.

XX Recombinant antibody fragment; rFab; botulinum; neurotoxin;  
KW Clostridium botulinum; detection; ds.  
XX Mus musculus.  
XX Key Location/Qualifiers  
FT 117..827  
FT /\*tag= a  
FT /product= "BotFab 5 antibody fragment, light chain"  
FT 847..1611  
FT /\*tag= b  
FT /product= "BotFab 5 antibody fragment, heavy chain"  
XX US5932449-A.  
PN 03-AUG-1999.  
XX 30-JAN-1997; 97US-0792824.  
XX 01-FEB-1996; 96US-0011013.  
PR 30-JAN-1997; 97US-0792824.  
XX (USSA ) US SEC OF ARMY.  
XX Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;  
WPI: 1999-492692/41.  
DR P-PSDB; AAY30116, AAY30117.  
XX Detection of botulinum toxin  
XX Claim 4; Columns 13-18; 24pp; English.

CC This sequence represents the cDNA coding for the light and heavy chain  
CC of BotFab 5, a murine recombinant antibody fragment (rFab) specific to  
CC botulinum toxin types A and B. A cDNA library was made from mouse mRNA  
CC isolated from mice immunised with human pentavalent toxoid. The cloned  
CC mouse heavy and light chains were expressed in phage display libraries  
CC and screened for their ability to bind to botulinum toxin types A or B.  
CC The clones were then isolated and sequenced. Botulinum neurotoxin is  
CC produced as several antigenically distinct serotypes (A-G) and is  
CC non-covalently associated with non-neurotoxic proteins. The rFab of  
CC this invention binds to the non-neurotoxic proteins that are found in  
CC neurotoxin complexes A and B. Such antibody fragments are able to  
CC act as immunosensors for detecting botulinum toxins in food and  
CC are also useful in health care and in military applications. They  
CC are less expensive to produce than monoclonal antibodies as they can be  
CC isolated from large scale bacterial cultures. Also, the affinity of an  
CC rFab may be altered by mutagenesis of its gene and subsequent screening  
CC of the expressed rFabs.

XX SQ Sequence 1672 BP; 439 A; 452 C; 403 G; 378 T; 0 other;

Query Match 63.9%; Score 626; DB 20; Length 1672;  
Best Local Similarity 92.9%; Pred. No. 4.6e-118;  
Matches 656; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 51 TGCTCACTCAGTCCCTGGCGTGTGCTGCTGTACAGGTGCCAGATGTGACATCC 110  
DB 130 TGCTCACTCAGTCCCTGGCGTGTGCTGCTGTACAGGTGCCAGATGTGACATCC 189  
QY 111 AGATGACTCAGTCTCCAGCTCCCTATCTGCTGCTGTGGGAGAACTGTACCATCACAT 170  
DB 190 AGATGACCCAGTCTCCAGCTCCCTATCTGCTGCTGTGGGAGAACTGTACCATCACAT 249  
QY 171 GTCGAGCAAGTGGGAATATTCAAAATATTAGCATGGTATCAGCAGACAGGAAAT 230  
DB 250 GTCGAGCAAGTGGGAATATTCAAAATATTAGCATGGTATCAGCAGACAGGAAAT 309  
QY 231 CTCTCAGCTCTGCTGCTATTCTGCAAAACCTTAGCAGATGCTGCTGATCAAGTTCA 290  
DB 310 CTCTCAGCTCTGCTGCTATTATGCAAAACCTTAGCAGATGCTGCTGATCAAGTTCA 369



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: June 23, 2003, 16:26:36 ; Search time 2633.04 Seconds  
(without alignments)  
10820.814 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 acacccttctgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_pl.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: em\_ba.\*

15: em\_fun.\*

16: em\_hum.\*

17: em\_in.\*

18: em\_mu.\*

19: em\_om.\*

20: em\_or.\*

21: em\_ov.\*

22: em\_ph.\*

23: em\_pl.\*

24: em\_ro.\*

25: em\_sts.\*

26: em\_un.\*

27: em\_vi.\*

28: em\_htg\_hum.\*

29: em\_htg\_inv.\*

30: em\_htg\_mus.\*

31: em\_htg\_rod.\*

32: em\_htg\_vrt.\*

33: em\_sy.\*

34: em\_htgo\_hum.\*

35: em\_htgo\_mus.\*

36: em\_htgo\_rod.\*

37: em\_htgo\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_rod.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	898	91.7	954	10	BC002112	BC002112 Mus muscu
2	881.2	90.0	942	10	BC019474	BC019474 Mus muscu
3	821	83.9	885	10	MMIG66L	X13187 Mouse mRNa
4	755	77.1	959	10	BC015292	BC015292 Mus muscu
5	751.8	76.8	1019	10	BC027418	BC027418 Mus muscu
6	751.8	76.8	1038	10	BC013496	BC013496 Mus muscu
7	751.6	76.8	972	10	AF466770	AF466770 Mus muscu
8	739.6	75.5	931	10	MMIG15K	X56394 Mouse mAB-1
9	733.6	74.9	998	9	S65921	S65921 anti-colore
10	689	70.4	721	10	MMU56412	U56412 Mus musculu
11	685.8	70.1	721	10	MMU56413	U56413 Mus musculu
12	685.4	70.0	943	10	MUSTGKAJ	J00560 mouse ig ka
13	683.8	69.8	943	10	MMIGK9	V00810 M.musculus
14	683.6	69.8	977	10	BC002035	BC002035 Mus muscu
15	679	69.4	974	10	MMABMT2	X79906 M.musculus
16	678.6	69.3	963	10	BC021781	BC021781 Mus muscu
17	677	69.2	882	6	E00398	E00398 Mouse anti-
18	672.8	68.7	985	10	MUSTGKBA	M63550 Mouse Ig re
19	669.6	68.4	943	10	BC028540	BC028540 Mus muscu
20	669.6	68.4	974	10	BC019760	BC019760 Mus muscu
21	666.2	68.0	956	10	MMKAPLI	X87231 M.musculus
22	666.2	68.0	1008	10	BC031498	BC031498 Mus muscu
23	665.6	68.0	957	10	MMU65535	U65535 Mus musculu
24	664.6	67.9	938	10	MMIGKL	X02816 Mouse mRNa
25	663.2	67.7	969	10	BC006643	BC006643 Mus muscu
26	654.4	66.8	993	10	AF466768	AF466768 Mus muscu
27	652	66.6	961	6	E08433	E08433 cDNA encodi
28	650.6	66.5	920	10	MMTMTVIGK	X67211 M.musculus
29	650.6	66.5	940	6	A44968	A44968 Sequence 24
30	650.6	66.5	940	6	I64459	I64459 Sequence 24
31	649.4	66.3	1034	10	BC028925	BC028925 Mus muscu
32	649.2	66.3	882	10	MMIGLCKA	X70424 M.musculus
33	634.2	64.8	5711	6	AX359934	AX359934 Sequence
34	634.2	64.8	5711	6	AX382148	AX382148 Sequence
35	634.2	64.8	5711	6	AX359939	AX359939 Sequence
36	634.2	64.8	5711	6	AX382153	AX382153 Sequence
37	620.8	63.4	927	10	MUSILC	DI7386 mRNa for mo
38	615.6	62.9	943	6	A22259	A22259 M.musculus
39	615.6	62.9	943	6	A77136	A77136 Sequence 4
40	615.6	62.9	943	6	AR029101	AR029101 Sequence
41	615.6	62.9	943	6	E33133	E33133 Humanized a
42	607.8	62.1	645	10	AF290569	AF290569 Mus muscu
43	598	61.1	882	6	A78883	A78883 Sequence 3
44	597.6	61.0	652	10	MSU00929	U00929 Mus MRL/lpr
45	593.8	60.7	862	10	RNU39609	U39609 Rattus norv

# ALIGNMENTS

RESULT 1	BC002112	BC002112	954 bp	mRNA	linear	ROD 07-AUG-2002
LOCUS	BC002112	Mus musculus, Similar to immunoglobulin kappa chain variable 8 (V8), clone MGC:6612	IMAGE:3488780, mRNA, complete cds.			
DEFINITION	BC002112	Mus musculus, Similar to immunoglobulin kappa chain variable 8 (V8), clone MGC:6612	IMAGE:3488780, mRNA, complete cds.			
ACCESSION	BC002112	Mus musculus, Similar to immunoglobulin kappa chain variable 8 (V8), clone MGC:6612	IMAGE:3488780, mRNA, complete cds.			
VERSION	BC002112.1	GI:12805290				
KEYWORDS	MGC					
SOURCE	house mouse					
ORGANISM	Mus musculus					
REFERENCE	1 (bases 1 to 954)					
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					

Tue Jul 1 18:40:58 2003

JOURNAL

Submitted (31-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 7 Row: k Column: 24  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES source

Location/Qualifiers  
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/db\_xref="taxon:10090"  
/map="C57BL/6J"  
/clone="MGC:6612 IMAGE:3488780"  
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/clone\_lib="NCI-CGAP\_Mam5"  
/lab\_host="DH108"  
/note="Vector: pCMV-SPORT6"  
27..731  
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/db\_xref="GI:12805291"  
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FGSYCOHFWGTPTFTGGGKFKVIGKRAADPTVSIIPPSSQELTSGGASVVCFLNPNY  
KPDINVKWKIDGSEKQNGVLSWTDQDSKSTYSMSSTLTLTKDEYERHNSYTCEATH  
KTSTSPVTKSFNRNEC"  
267 a 257 c 203 g 227 t

CDS

267 a 257 c 203 g 227 t

BASE COUNT ORIGIN

Query Match 91.7%; Score 998; DB 10; Length 954;  
Best Local Similarity 96.3%; Pred. No. 2.1e-238;  
Matches 919; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
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1 CAGCCTCAGTATGATCACACAGTATGCTGCTCAGTCTCAGTCTCGGTGCTGC 60  
78 TCGTCTGCTTACAGTCCGAGTCCAGATCCAGATGACTGCTCCAGCTCCCTAT 137  
61 TCGTCTGCTTACAGTCCGAGTCCAGATCCAGATGACTGCTCCAGCTCCCTAT 120  
138 CTGCATCTGTGGGAGAACTGTCAACATCACATGTCTGAGCAAGTGGGAATATCAAAAT 197  
121 CTGCTCTGTGGGAGAACTGTCAACATCACATGTCTGAGCAAGTGGGAATATCAAGTA 180  
198 ATTTAGCATGGTATCAGCAGACAGGAGAAATCTCCTCAGCTCTGCTTATTCGAA 257  
181 ATTTAGCATGGTATCAGCAGACAGGAGAAATCTCCTCAGCTCTGCTTATTCGAA 240  
258 AAACCTTAGCATGGTGTGCCATCAGGTTTCAAGTTCAGTGGCAGTGGATCAGGAACACATAT 317  
241 CAAACTTAGCATGGTGTGCCATCAGGTTTCAAGTTCAGTGGCAGTGGATCAGGAACACATAT 300  
318 CTCTCAAGATCAACACCTTCGAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTT 377

1  
301 CCCCTCAGATCAACAGCCTGCAGTCTGAAGATTTGGAGTTATTACTGTCAACATTTT 360  
378 GGAGTACTCCCTACACAGTTCGGAGGGGGACCAAGCTGGAAATAAACGGGCTGATGCTG 437  
361 GGGTACTCCGTTTACATTCGGAGGGGGACCAAGTGGGATAAACGGGCTGATGCTG 420  
438 CACCAACTGTATTCATCTCCACATCCAGTGGAGTGAACATCTGGAGTGGCTCAG 497  
421 CACCAACTGTATTCATCTCCACATCCAGTGGAGTGAACATCTGGAGTGGCTCAG 480  
498 TCGTGTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGGAGATTTGATG 557  
481 TCGTGTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGGAGATTTGATG 540  
558 CCAGTGAAGCAGCAAAATGCGTCTTGAACAGTTGGAGTGGATGATCAGGACAGCAACGCA 617  
541 GCAGTGAAGCAGCAAAATGCGTCTTGAACAGTTGGAGTGGATGATCAGGACAGCAACGCA 600  
618 CCTACAGATGAGCAGCAGCCCTCAGCTTGAACAGGACGAGTATGAACACATACAGCT 677  
601 CCTACAGATGAGCAGCAGCCCTCAGCTTGAACAGGACGAGTATGAACACATACAGCT 660  
678 ATACCTGTGAGGCCACTCACAGACATCAATTCACCCATTTGTCAGAGCTTCAACAGCA 737  
661 ATACCTGTGAGGCCACTCACAGACATCAATTCACCCATTTGTCAGAGCTTCAACAGCA 720  
738 ATGAGTGTAGAGACAAAGTCTCTGAGAGCGCCACACAGCTCCCGAGCTCCATCTATC 797  
721 ATGAGTGTAGAGACAAAGTCTCTGAGAGCGCCACACAGCTCCCGAGCTCCATCTATC 780  
798 TTCCCTCTTAAGTCTTGGAGGCTTCCCCACAAAGCAGCTTACACATTTTCGGTGTCTCA 857  
781 TTCCCTCTTAAGTCTTGGAGGCTTCCCCACAAAGCAGCTTACACATTTTCGGTGTCTCA 840  
858 AACCTCTCTCCACCT 917  
841 AACCTCTCTCCACCT 900  
918 TTTCAGAAAAATATTCAATAAAGTGAAGTCTTTGCAAAAAAAGAAAAA 971  
901 TTTCAGAAAAATATTCAATAAAGTGAAGTCTTTGCAAAAAAAGAAAAA 954

RESULT 2  
BC019474 942 bp mRNA linear ROD 07-AUG-2002  
LOCUS MUS musculus, clone MGC:28604 IMAGE:4217320, mRNA, complete cds.  
DEFINITION BC019474.1 GI:18044484  
ACCESSION BC019474.1  
VERSION  
KEYWORDS MGC.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 942)  
Strausberg, R.  
Direct Submission  
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

REMARK COMMENT





Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 959)  
Strausberg, R.  
Direct Submission  
Submitted (01-OCT-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@exil1.stanford.edu](mailto:mcd@exil1.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 25 Row: g Column: 15  
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES  
source  
1. .959  
Location/Qualifiers  
identity to person.

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  /map="FVB/N"
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    /clone_lib="NCI_CGAP_Co2
    /lab_host="DH10B"
  /note="vector: pCMV-SPORT
13. .717
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5

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KTSTPTVASFNRNEC	200 °	253 °	188 °	230 °

BASE COUN  
CITY

ORIGIN	Query Match	Score 755;	DB 10;	Length 959;
Subtotal Similarity	87.8%;	pred. No. 1.1e-198;		

**Qy**

Matches	824;	Conservative	0;	Mismatches	115;	Indels	0;	Gaps	0;
Best Local Similarity	67.3%								
Query	41 GTATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGTGCCTACAGGTGCCAGA 100                                 								

[illegible][illegible][illegible][illegible]

RESULT 4	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	BC015292	Mus musculus, clone MGC:19136 IMAGE:4216659, mRNA	959 bp	linear	ROD 07-AUG-2002		
	BC015292	Mus musculus, clone MGC:19136 IMAGE:4216659, mRNA, complete cds.					





QY	341	CCTGAAGATTTTGGAGGATTATTACTGTCACAAATTTTGGAGTACTCCGTACAGTTCGGA	400
Db	338	CAAGAAGATGTTGCCACTACTCTTTTGCCAAACAGGCTTATACGCTTCCGTACAGTTCGGA	397
QY	401	GGGGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCCA	460
Db	398	GGGGGACCAAGCTGGAATAAAAGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA	457
QY	461	CCATCCAGTGAGCAGTTAAACATCTTGAGGTGCTCAGTCGTGTGCTCTTGGACAACTTC	520
Db	458	CCATCCAGTGAGCAGTTAAACATCTTGAGGTGCTCAGTCGTGTGCTCTTGGACAACTTC	517
QY	521	TACCCCAAAGACATCAATGTCAAGTGGAGATTGATGCGAGTGAACGACAAATGGCGTC	580
Db	518	TACCCCAAAGACATCAATGTCAAGTGGAGATTGATGCGAGTGAACGACAAATGGCGTC	577
QY	581	CTGAACAGTTGGAGCTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCTC	640
Db	578	CTGAACAGTTGGAGCTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCTC	637
QY	641	ACGTTGACCAAGGACGAGTATGAACGACATCAACAGCTATACCTGTGAGGCCACTACAAG	700
Db	638	ACGTTGACCAAGGACGAGTATGAACGACATCAACAGCTATACCTGTGAGGCCACTACAAG	697
QY	701	ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGACACAAAGTCC	760
Db	698	ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGACACAAAGTCC	757
QY	761	TGAGAGCGCACCAACAGCTCCCGAGTCCATCTCTTCCCTTCAAGGCTCTGGAGGC	820
Db	758	TGAGAGCGCACCAACAGCTCCCGAGTCCATCTCTTCCCTTCAAGGCTCTGGAGGC	817
QY	821	TTCCCCACAGCGACCTACAGCTGTTCGGGTGCTCCAAACCTCCTCCCACTCTCTCTC	880
Db	818	TTCCCCACAGCGACCTACAGCTGTTCGGGTGCTCCAAACCTCCTCCCACTCTCTCTC	877
QY	881	CT	940
Db	878	CT	937
QY	941	TGAGTCTTTGGCAAAAAAATAAAAAAAAAAAAAA	975
Db	938	TGAGTCTTTGGCAAAAAAATAAAAAAAAAAAAAA	972
RESULT 8			
MMIG15K			
LOCUS		931 bp	linear
DEFINITION		Mouse mAB-15C5 mRNA for immunoglobulin kappa chain.	ROD 23-MAR-1995
ACCESSION		X56394	
VERSION		X56394.1	GI:51622
KEYWORDS		gamma-immunoglobulin; immunoglobulin.	
SOURCE		Mus musculus	
ORGANISM		Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE			
AUTHORS		Vandamme, A.M.I.	
TITLE		Submitted (06-JUL-1990)	
JOURNAL		Center for Thrombosis and Vascular Research, Herestraat 49, B-3000 Leuven	
REFERENCE			
AUTHORS		Vandamme, A.M., Bulens, F., Bernar, H., Nelles, L., Lijnen, R.H. and Collen, D.	
TITLE		Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer	
JOURNAL		Eur. J. Biochem. 192 (3), 767-775 (1990)	
MEDLINE		91006173	
PUBMED		2209622	
COMMENT		rearranged; zap1;	

Tue Jul 1 18:40:58 2003

This sequence is of c DNA corresponding tomRNA for the antibody  
MA1515 directed against crosslinked human fibrin fragment D-dimer  
Data kindly reviewed (27-NOV-1990) by Vandamme A.M.

# FEATURES

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5. .709  
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5. .64  
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389. .706  
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V\_region  
V\_segment  
C\_region  
BASE COUNT 258 a 240 c 202 g 231 t  
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Best Local Similarity 87.2%; Pred. No. 2.2e-194;  
Matches 811; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
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2 GACATGAGGACCCCTCTCAGTTCTTGGAACTCTTGTGCTGTGGTTCCAGGTATCAAA 61  
1  
101 TGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGTCATCTGTGGGAAACTGTC 160  
1  
62 TGTGACATCAAGATGACCCAGTCTCCATCTCCATCTGTCATCTGTCATCTGAGGAGAGATC 121  
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161 ACCATCACATGTCGAGCAAGTGGGAATATTCAAATATTTAGCATGTTATCAGCAGACA 220  
1  
122 ACTGTCACTTGCAGGGGAGTCCAGGACATTAATAGCTATTTAAAGTCCAGCAGAAA 181  
1  
221 CAGGAAATCTCTCAGTCTCTGCTATCTCCAAAACCTTTAGCAGATGTTGTGCCA 280  
1  
182 CCAGGAAATCTCTCAGGACCCCTGATCTACCGTGGAAACAGATTGGTTGCTGGGTCCTCA 241  
1  
281 TCAGGTTTCAGTGCAGTGGATGAGGACAAATATCTCTCAAGATCAACAGCCTGCAG 340  
1  
242 TCAAGGTTTCAGTGCAGTGGATGAGGACAAATATCTCTCACCATCAGCAGCCTGGAG 301  
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341 CCTGAAGATTTTGGGAGTTATCTACTGTCAACATTTTTGGAGTACTCCGTACAGTTCGA 400  
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362 TCGGGACAAAGTTGGAATAAACGGGCTGATGCTGCACCAACTGTATCATCTTCCCA 421  
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461 CCATCACTGAGCAGTTACATCTCGAGGTGCCTCAGTCTGCTGCTTCTTGAACAACCTTC 520  
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422 CCATCACTGAGCAGTTACATCTCGAGGTGCCTCAGTCTGCTGCTTCTTGAACAACCTTC 481  
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QY 761 TGACAGCGCACCCAGCTCCCGAGCTCCCATCTTCTTCCCTTCTAAGGTCCTTGGAGGC 820  
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Db 902 TGAGTCTTTGGCAAAAAAAGAAAAA 931

## RESULT 9

S65921  
LOCUS  
DEFINITION  
anti-colorectal carcinoma light chain-glycoprotein CANAG-50  
specific IgG1 kappa [human, 19.9 hybridoma, antibody 1116NS19.9,  
mRNA, 998 nt].  
S65921  
VERSION  
S65921.1 GI:425519  
KEYWORDS  
Homo sapiens 19.9 hybridoma antibody 1116NS19.9.  
SOURCE  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 998)  
Tongue,D.W., Hennem,J.F., Greene,A.R., Lee,I.D. and Edge,M.D.  
Cloning and characterization of 1116NS19.9 heavy and light chain  
cDNAs and expression of antibody fragments in Escherichia coli  
Year Immunol. 7, 56-62 (1993)  
JOURNAL  
MEDLINE  
8372513  
PUBMED  
REMARK  
GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 138017] from the original journal article.  
This sequence comes from Fig. 2.  
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/db\_xref="taxon:9606"  
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80. .790  
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This sequence comes from Fig. 2"  
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[illegible]







SOURCE mouse cdna to myeloma mopc21 mrna; cdna to myeloma p3 (derived from mopc21) mrna; cdna to myeloma mopc149 mrna; cdna to myelomas mopc41a, mopc603, s107 & hpc76 mrna (see comment).

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 899 to 943)

AUTHORS Milstein,C., Brownlee,G.G., Cartwright,E.M., Jarvis,J.M. and Proudfoot,N.J.

TITLE Sequence analysis of immunoglobulin light chain messenger RNA

JOURNAL Nature 252 (5482), 354-359 (1974)

MEDLINE 75045384

PUBMED 4473725

REFERENCE 2 (bases 857 to 943)

AUTHORS Hamlyn,P.H., Gillam,S., Smith,M. and Milstein,C.

TITLE Sequence analysis of the 3' non-coding region of mouse immunoglobulin light chain messenger RNA

JOURNAL Nucleic Acids Res. 4 (4), 1123-1134 (1977)

MEDLINE 77193574

PUBMED 405661

REFERENCE 3 (bases 412 to 943)

AUTHORS Hamlyn,P.H., Brownlee,G.G., Cheng,C.C., Gait,M.J. and Milstein,C.

TITLE Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA sequencing

JOURNAL Cell 15 (3), 1067-1075 (1978)

MEDLINE 79084137

PUBMED 103625

REFERENCE 4 (bases 607 to 676)

AUTHORS Seidman,J.G., Edgell,M.H. and Leder,P.

TITLE Immunoglobulin light-chain structural gene sequences cloned in a bacterial plasmid

JOURNAL Nature 271 (5645), 582-585 (1978)

MEDLINE 78092449

PUBMED 414143

REFERENCE 5 (bases 841 to 943)

AUTHORS Gough,N.M., Cory,S. and Adams,J.M.

TITLE Identical 3' non-coding sequences in five mouse Ig kappa chain mRNAs favour a unique C kappa gene

JOURNAL Nature 281 (5730), 394-396 (1979)

MEDLINE 80011674

PUBMED 113684

REFERENCE 6 (bases 1 to 943)

AUTHORS Hamlyn,P.H., Gait,M.J. and Milstein,C.

TITLE Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing

JOURNAL Nucleic Acids Res. 9 (18), 4485-4494 (1981)

MEDLINE 82059477

PUBMED 6170937

COMMENT Sequences from myelomas mopc149, hpc76, and mopc603 are included with this locus even though they are different from the main sequence myeloma (mopc21) because the only portion of their mRNAs which has been sequenced is in the c region, which is known to be the same in all kappa mRNAs.

The sequence reported here is a productive rearrangement of myeloma mopc21. The 5' untranslated region (5'ut) of the mopc21 mrna is unusual in that it probably consists of only three bases. [6] could not be absolutely certain that the full 5'ut was obtained, but based upon other results using the same sequencing technique, [6] feels that it is probable that a 3bp 5'ut is correct. This is further supported by the discovery of another kappa v gene which has a 3 bp 5' ut <musikal>. mopc21 has also undergone an unproductive rearrangement <musikal>.

The germline variable region of mopc21 has not been sequenced, and its joining region is j2. [5] reports the comp. strand, loci beginning <musikv> for germline kappa variable regions; see loci beginning <musikal> for rearranged kappa genes; and see loci beginning <musikic> for the kappa germline joining and constant regions. In the sites table cdr-complementarity determining region and fr-framework region.

EMBL features not translated to GenBank features:

key from to description

CDS 4 732 reading frame

FEATURES

source

mouse cdna to myeloma mopc21 mrna [1],[3]; cdna to myeloma p3 (derived from mopc21) mrna [2],[5],[6]; cdna to myeloma mopc149 mrna; cdna to myelomas mopc41a, mopc603, s107 & hpc76 mrna [5].

location/Qualifiers

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/db\_xref="taxon:10090"

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/product="kappa mopc21 mrna"

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/note="kappa mopc21 coding sequence"

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/note="kappa mopc21 signal sequence"

91..732

/product="kappa mopc21 mature peptide coding region"

BASE COUNT 255 a 254 c 207 g 222 t 5 others

ORIGIN 5' end of mrna (see comment).

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Best Local Similarity 85.2%; Pred.No. 2.5e-179;  
Matches 764; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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QY 116 ACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTCCACCATCATGTCGA 175  
Db 103 ACCCAATCTCCAAATCCATGTCATGTCAGTAGGAGAGAGGTCCACCTTGACCTGCAAG 162

QY 176 GCAAGTGGGAATATCAAAATTTATAGCATGGTATCAGACAGACAGAGGAAATCTCT 235  
Db 163 GCCAGTGAGATGGTGTACTTATGTTTTCGTTATCAACAGAAACACAGCAGTCTCT 222

QY 236 CAGTCTCTGGTCTATCTGCAAAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAAGTGGC 295  
Db 223 AAACGTGTATATGGGCAATCCACGGTACACTGGGGTCCCNATCGCTTTCACAGGC 282

QY 296 AGTGGATCAGGAACAATATTTCTCAAGATCAACGCCCTGCAGCCTGAAGATTTGGG 355  
Db 283 AGTGGATCTCAACAGATTTTCACTCTGACCATCAGCAGTGTGAGGCTGAAGACCTTGCA 342

QY 356 AGTTATTACTGTCAACATTTTGGAGTACTCCGTACACGTTCCGGAGGGGGACCAAGCTG 415  
Db 343 GAATATCAGTGTGCACAGGGTTACAGTATCCGTACAGTTCGGAGGGGGACCAAGCTG 402

QY 416 GAAATAAACGGCTGATGCTGCACCAACTGTATCTTCCACCATCCAGTGCAGCAG 475  
Db 403 GAAATAAACGGCTGATGCTGCACCAACTGTATCTTCCACCATCCAGTGCAGCAG 462

QY 476 TTAACATCTCGAGGTGCTCAGTCGTGTCTTGAACAATTTCTACCCCAAGACATC 535  
Db 463 TTAACATCTCGAGGTGCTCAGTCGTGTCTTGAACAATTTCTACCCCAAGACATC 522

QY 536 AATGTCAAGTGAAGATTGATGGCAGTGAACGACAAATGGCGTCTTGACAGTTGACT 595  
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reading frame variable part  
reading frame joining part  
reading frame constant part  
listed as T in RNA, may be U  
listed as T in RNA, may be U  
polyA addition site Complete source

information:



VERSION	BC002035.1	GI:12805154
KEYWORDS	MGC.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 977)	
JOURNAL	Strausberg, R.	
	Direct Submission	
	Submitted (31-JAN-2001) National Institutes of Health, Mammalian	
	Gene Collection (MGC), Cancer Genomics Office, National Cancer	
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
	USA	
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	
COMMENT	Contact: MGC help desk	
	Email: <a href="mailto:cgabbs@email.nih.gov">cgabbs@email.nih.gov</a>	
	Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys	
	cDNA Library Preparation: Life Technologies, Inc.	
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome	
	Center, Stanford University School of Medicine, Stanford, CA 94305	
	Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a>	
	Contact: (Dickson, Mark) <a href="mailto:mcdepaxil.stanford.edu">mcdepaxil.stanford.edu</a>	
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A. and Myers,	
	R. M.	

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK plate: 8 Row: c Column: 13  
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

**FEATURES**  
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COUNT	261 a 264 c 209 g 243 t

BASE COUNT  
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Matches	783;	Conservative	0;	Mismatches	124;	Indels	15; Gaps 1;
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56	CTGTTGGTGCATGGTTCTGGATCTCTCCAGCAGTGTGTTGATGACCCAACT	115					
125	CCAGCTCCCTATCTGCATCTGTGGGAGAACTGTCACCATCATCTCAGAGAAATGGG	184					
116	CCACTCTCCCTGCTGTCAGTCTTTGGAGATCAAGCCTCCATCTTTCGATCTAGTTCAG	175					
185	AATATTCAAAT-----TATTAGCATGTTATCAGCACACACAGGAAAA	229					
176	AGCATTTGATCATAGTATATGAGAAACACCTATTTAGAAATGGTACCTGCAGAAACAGGCCAG	235					
230	TCTCCTCAGCTCCTGGTCTATTTCGAAAAACCTTAGCAGATGGTGTGCATCAAGGTTTC	289					

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RESULT 15	MMAABMST2		
LOCUS	MMAABMST2		
DEFINITION	M.musculus mRNA for monoclonal antibody MST2 light chain. X79906		
ACCESSION	X79906		
VERSION	.1 GI:1556423		
KEYWORDS	kappa light chain; light chain; monoclonal antibody.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;		Cranialta; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Mus.
REFERENCE	Janon,K. Unpublished		
JOURNAL	(bases 1 to 974)		
AUTHORS	Direct Submission		
TITLE	K. Janon, Commissariat a l'energie, atomique, Diep Bat. 152 CEN, Saclay, 91191 Gif/Yvette Cedex, FRANCE		
FEATURES	Location/Qualifiers . . . 974		
source			

Tue Jul 1 18:40:58 2003

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QY  
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933 CAATAAAGTGAGTCTTTCGAAAAAAGAAAAAAGAAAAA 971  
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Job time : 2639.04 secs

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[illegible]

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T	01-MAR-2002	(TrEMBLrel. 20, Created)		
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S	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)		
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	Mus musculus (Mouse).			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.			
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	Straussberg R.;			
	Submitted (DEC-2001) to the EMBL/GenBank/SwissProt database			

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Pfam: PF000047; Ig; 2.
SMART: SM00409; Ig; 2.
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SMART: SM00406; IGV; 1.
PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

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RESULT 11

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AC Q8TCD0; 45.2%; Score 558; DB 11; Length 298;

DT 01-JUN-2002 (TREMELrel. 21, Created)

DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Hypothetical 26.2 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RA Strausberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC022362; AAH22362.1; -

DQ Hypothetical protein.

SW SEQUENCE 239 AA; 26234 MW; FACEDEC3A3B03871D CRC64;

Query Match 54.2%; Score 668.5; DB 4; Length 239;

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QY 56 YQQTQKSPOLLVYSAKTLADGVPSPRSGSGSTQYSLKINSLOPEDFGSYQHFWSPT 115

Db 61 FQRPQSPRLIYKVNDSGVPDRFSGSGSTDFTLKTRVEAEDGVYFCMQGTHWP 120

QY 116 YTFGGTQKLEIKRADAAPTVSIFFPPSSQSLTSGGASVGCFLNNFYKPDINVKKIDGSR 175

Db 121 STFGQGTQKLEIKRTVAAPSVFFPPSPDEQLKSTASVVCLLNFFPREAKVQKVDNALQ 180

QY 176 QNGVLNSWTDQDSDKSTYSMSSTLTITKDEYERHNSYTCEATHKTSPTIVKSFNRNEC 234

Db 181 SGNQSFVTEQDSDKSTYSLSSTLTLSKADYKHKYVACEVTHOGLSPVTKSFNRGEC 239

RESULT 12

Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0; 45.0%; Score 555; DB 11; Length 109;

DT 01-MAY-2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)

DE CN 8 scfv.

DE CN 8 scfv.

DE CN 8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C; TISSUE=SPLREN;

RC MEDLINE=20183931; PubMed=10706631;

RA Shinohara N., Demura T., Fukuda H.;

YT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."

DE Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

EMBL; AB036341; BAA88633.1; -

RC HSSP; P01607; IREI.

RC InterPro; IPR03006; Ig\_MHC.

RC Pfam; PF00047; Ig; 2.

RC SMART; SM00406; IGV; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 45.2%; Score 558; DB 11; Length 298;

Best Local Similarity 89.1%; Pred. No. 1.1e-42;

Matches 106; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 17 GARCDIQMTQSPASLSASVGETVTITCRASGNIQYSLKINSLOPEDFGSYQHFWSPT 135

Db 169 GGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQKQKSPOLLVYNAKTLAD 228

QY 77 GVPSPRSGSGSTQYSLKINSLOPEDFGSYQHFWSPT 135

Db 229 GVPSPRSGSGSTQYSLKINSLOPEDFGSYQHFWSPT 287

RESULT 13

Q920E6 PRELIMINARY; PRT; 109 AA.

AC Q920E6; 45.0%; Score 555; DB 11; Length 109;

DT 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)

DE Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).

DE Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;

RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307938; AAL09422.1; -

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig; 1.

FT NON\_TER 1

FT NON\_TER 109

FT NON\_TER 109

SQ SEQUENCE 109 AA; 11943 MW; DADBF98E05DD1501 CRC64;

Query Match 45.0%; Score 555; DB 11; Length 109;

Best Local Similarity 96.3%; Pred. No. 5.1e-43;

Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNIQYSLKINSLOPEDFGSYQHFWSPT 80

Db 1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQKQKSPOLLVYNAKTLADGVP 60

QY 81 RFGSGSGSTQYSLKINSLOPEDFGSYQHFWSPT 129

Db 61 RFGSGSGSTQYSLKINSLOPEDFGSYQHFWSPT 109

RESULT 14

Q8TBC9 PRELIMINARY; PRT; 233 AA.

AC Q8TBC9; 45.0%; Score 555; DB 11; Length 109;

DT 01-JUN-2002 (TREMELrel. 21, Created)

DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Hypothetical 24.9 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PRIMARY B-CELLS;

RC Strausberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC022823; AAH22823.1; -

KW Hypothetical protein.

us-09-770-916-4.rspt

Search completed: June 18, 2003, 16:46:08  
Job time : 34.1938 secs

Tue Jul 1 18:41:11 2003

SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;  
Query Match 36.5%; Score 450; DB 4; Length 233;  
Best Local Similarity 40.9%; Pred. No. 5,3e-33;  
Matches 97; Conservative 46; Mismatches 86; Indels 8; Gaps 6;  
1 MSVLTQVLALLLLLTGARCIDIOMTQSPASLSASVGETVTTTCRASGNIQNYLAWYQQTQ 60  
1 MAWPLLLPLTL-CTGSEASYELTQ-PPSVSVSPGTARITCSGDALPKOYAYWYQKP 58  
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWS--TPYTF 118  
59 GQAPLVIIYKNERPSGIPERFSGSGSTTTLTISGVQAEADYCYOSADSSGTYWVF 118  
119 GGGTKLEI-KRADAAPTIVSIIPSPSEQLTSGGASVVCFLNNFYKPDINVKWKIDGSRQN 177  
119 GGGTKLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKA 178  
178 GVLSNWTDDSKDSTYSMSSTLTITKDEYERHNSYTCETHKHTSTSPIVKSFNRNEC 234  
179 GV-ETTPSKQSNKNKYAASSLSLTPEQWKSFKSHKSCQVTHEGST--VEKTVAPTEC 232

RESULT 15

8WTU6 PRELIMINARY; PRT; 237 AA.  
D Q8WTU6  
C Q8WTU6;  
T 01-MAR-2002 (TrEMBLrel. 20, Created)  
T 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
E Hypothetical 24.9 kDa protein.  
S Homo sapiens (Human).  
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=TONSIL;  
Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; BC022098; AAH22098.1;  
InterPro; IPR003599; Ig.  
InterPro; IPR003597; Ig-cl.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 2.  
SMART; SM00409; IG; 2.  
SMART; SM00407; IGcl; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
Hypothetical protein.  
SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;  
Query Match 35.5%; Score 437.5; DB 4; Length 237;  
Best Local Similarity 42.6%; Pred. No. 7.4e-32;  
Matches 100; Conservative 41; Mismatches 83; Indels 11; Gaps 8;  
7 VLALLLLLTGARCIDIOMTQSPASLSASVGETVTTTCR-ASGNI-QNY-LAWYQQTQGS 63  
6 LLLTLAHTCGSWAGSVLTQ-PPSVSGAPGORVTITCTGSSNIGAGYDVHWHYQQLPGTA 64  
64 POLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHF---WSTPYTFGG 120  
65 PKLLIYGNRNPSGVPDRFSGSGTSASLATLGQAEADYCYOSDYSLASGVFGG 124  
121 GTKLEI-KRADAAPTIVSIIPSPSEQLTSGGASVVCFLNNFYKPDINVKWKIDGSRQNGV 179  
125 GTKLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGV 184  
180 LNSWTDDSKDSTYSMSSTLTITKDEYERHNSYTCETHKHTSTSPIVKSFNRNEC 234  
185 -ETTPSKQSNKNKYAASSLSLTPEQWKSFKSHKSCQVTHEGST--VEKTVAPTEC 236

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:52 ; Search time 9.5309 seconds  
(without alignments)  
1018.315 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVLALLLLWLTGARC.....EATHKTSTSPVKSFNRNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	586	47.5	115	1	KV5C_MOUSE	P01635 mus musculus
2	565	45.8	106	1	KAC_MOUSE	P01837 mus musculus
3	481	39.0	106	1	KACA_RAT	P01836 rattus norv
4	481	39.0	108	1	KVSD_MOUSE	P01636 mus musculus
5	466	37.8	106	1	KACB_RAT	P01835 rattus norv
6	453	36.7	129	1	KV1W_HUMAN	P04431 homo sapien
7	436	35.3	129	1	KV1X_HUMAN	P04432 homo sapien
8	409	33.1	117	1	KV1J_HUMAN	P01602 homo sapien
9	402	32.6	128	1	KV5E_MOUSE	P01637 mus musculus
10	401	32.5	108	1	KV1S_HUMAN	P01611 homo sapien
11	399	32.3	108	1	KV1H_HUMAN	P01600 homo sapien
12	396	32.1	108	1	KV1C_HUMAN	P01595 homo sapien
13	395	32.0	108	1	KV1O_HUMAN	P01607 homo sapien
14	392	31.8	108	1	KV1V_HUMAN	P04430 homo sapien
15	392	31.8	117	1	KV1I_HUMAN	P01601 homo sapien
16	388	31.4	108	1	KV1L_HUMAN	P01610 homo sapien
17	387	31.4	108	1	KV4C_HUMAN	P06314 homo sapien
18	386	31.3	134	1	KV3K_HUMAN	P06311 homo sapien
19	384	31.1	128	1	KV3L_HUMAN	P06310 homo sapien
20	381	30.9	108	1	KV1N_HUMAN	P06311 homo sapien
21	381	30.9	108	1	KV1Y_HUMAN	P06311 homo sapien
22	378	30.6	108	1	KV1E_HUMAN	P06311 homo sapien
23	377.5	30.6	129	1	KV3H_HUMAN	P06311 homo sapien
24	375.5	30.4	133	1	KV4B_HUMAN	P06311 homo sapien
25	375	30.4	108	1	KV1B_HUMAN	P06311 homo sapien
26	374.5	30.4	129	1	KV3M_HUMAN	P06311 homo sapien
27	374	30.3	108	1	KV1P_HUMAN	P06311 homo sapien
28	373.5	30.3	129	1	KV3L_HUMAN	P06311 homo sapien
29	372.5	30.2	107	1	KV1D_HUMAN	P06311 homo sapien
30	371	30.1	108	1	KV1Q_HUMAN	P06311 homo sapien
31	369	29.9	108	1	KV1F_HUMAN	P06311 homo sapien
32	367	29.7	108	1	KV1M_HUMAN	P06311 homo sapien
33	367	29.7	130	1	KV5G_MOUSE	P01639 mus musculus

34	366	29.7	108	1	KV1G_HUMAN	P01599 homo sapien
35	364	29.5	108	1	KV1A_HUMAN	P01593 homo sapien
36	362	29.3	108	1	KV1K_HUMAN	P01603 homo sapien
37	360	29.2	115	1	KV5F_MOUSE	P01638 mus musculus
38	356	28.8	114	1	KV4A_HUMAN	P01625 homo sapien
39	351	28.4	136	1	KV5B_MOUSE	P01634 mus musculus
40	350.5	28.4	109	1	KV1T_HUMAN	P01612 homo sapien
41	350	28.4	106	1	KAC_HUMAN	P01834 homo sapien
42	350	28.4	108	1	KV5J_MOUSE	P01643 mus musculus
43	350	28.4	149	1	KV5A_MOUSE	P01646 mus musculus
44	348	28.2	108	1	KV5M_MOUSE	P01646 mus musculus
45	345	28.0	108	1	KV5O_MOUSE	P01648 mus musculus

ALIGNMENTS

RESULT 1

KV5C\_MOUSE

ID KV5C\_MOUSE STANDARD; PRT: 115 AA.

AC P01635;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-V region K2 precursor (fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ON NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8015999; PubMed=6767723;

RA Nishio Y., Leder P.;

RT "Organization and complete sequence of identical embryonic and

plasmacytoma kappa V-region genes."

RL J. Biol. Chem. 255:3691-3694 (1980).

CC -1- MISCELLANEOUS: THE GENE WAS ISOLATED AND SEQUENCED SEPARATELY FROM

TWO DIFFERENT SOURCES, EMBRYOS AND CULTURED PLASMACYTOMA CELLS

THAT SECRETE THE SIMILAR KAPPA CHAIN MOPC 149.

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CC EMBL; V00778; CAA24155.1; -

DR PIR; A01918; KVMK2.

DR HSSP; P01607; IREI.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL

FT CHAIN 1 20

FT DOMAIN 21 >115

FT DOMAIN 21 >115

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 >115

FT DISULFID 43 108

FT NON\_TER 115 115

SQ SEQUENCE 115 AA; 12581 MW; 4F41E3D40C539DEC CRC64;

Query Match

Best Local Similarity 97.4%; Score 586; DB 1; Length 115;

Matches 112; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVLTVLALLLLWLTGARCIDIQTSPASLSASVGETVTITCRASGNITQNYLAWTQQTQ 60

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/anne](http://www.isb-sib.ch/announce/)

1 MSVLQVALLLWLTGARDIQMTQSPASLSASVGETVITCRASGNLHNTLAWTQQKQ 60  
61 GKSPQLLVYSAKTLADGVPSRSGSGGTQYSLKINSLOPEDFGSYICQHFWSWP 115  
61 GKSPQLLVYNAKTLADGVPSRSGSGGTQYSLKINSLOPEDFGSYICQHFWSWP 115

RESULT 2  
AC\_MOUSE  
D KAC\_MOUSE STANDARD; PRT; 106 AA.  
C P01837;  
T 21-JUL-1986 (Rel. 01, Created)  
T 21-JUL-1986 (Rel. 01, Last sequence update)  
T 16-OCT-2001 (Rel. 40, Last annotation update)  
E Ig kappa chain C region.  
S Mus musculus (Mouse).  
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
X NCBI\_TaxID=10090;  
[1]  
SEQUENCE (MOPC 21).  
MEDLINE=73053310; PubMed=4638343;  
A Swasti J., Milstein C.;  
T "The complete amino acid sequence of a mouse kappa light chain.";  
L Biochem. J. 128:427-444(1972).  
[2]  
DISULFIDE BONDS (MOPC 21).  
MEDLINE=73008889; PubMed=5073237;  
A Swasti J., Milstein C.;  
T "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
L Biochem. J. 126:837-850(1972).  
[3]  
SEQUENCE FROM N.A., AND REVISIONS TO 53-59.  
MEDLINE=79084137; PubMed=103625;  
X Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;  
T "Complete sequence of constant and 3' noncoding regions of an  
X immunoglobulin mRNA using the dideoxynucleotide method of RNA  
X sequencing.";  
L Cell 15:1067-1075(1978).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=62059477; PubMed=6170937;  
X Hamlyn P.H., Gait M.J., Milstein C.;  
T "Complete sequence of an immunoglobulin mRNA using specific priming  
X and the dideoxynucleotide method of RNA sequencing.";  
L Nucleic Acids Res. 9:4485-4494(1981).  
[5]  
SEQUENCE FROM N.A.  
MEDLINE=81191915; PubMed=6262318;  
X Max E.E., Maizel J.V. Jr., Leder P.;  
T "The nucleotide sequence of a 5.5-kilobase DNA segment containing the  
X mouse kappa immunoglobulin J and C region genes.";  
L J. Biol. Chem. 256:5116-5120(1981).  
[6]  
SEQUENCE FROM N.A.  
MEDLINE=81198949; PubMed=6785724;  
X Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;  
T "DNA sequence of the constant gene region of the mouse immunoglobulin  
X kappa chain.";  
L Nucleic Acids Res. 9:971-981(1981).  
[7]  
SEQUENCE FROM N.A.  
MEDLINE=88329081; PubMed=3138116;  
X de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;  
T "Expression in non-lymphoid cells of mouse recombinant immunoglobulin  
X directed against the tumour marker human placental alkaline  
X phosphatase.";  
L Eur. J. Biochem. 176:287-295(1988).  
-----  
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the European Bioinformatics Institute. There are no restrictions on its

Query Match 45.8%; Score 565; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.9e-39;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SQ SEQUENCE 106 AA; 11778 MW; 4B5IFF5EF49ABE5 CRC64;  
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106  
SQ SEQUENCE 106 AA; 11778 MW; 4B5IFF5EF49ABE5 CRC64;

QY 129 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQGVLSWTQDQS 188  
DB 1 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQGVLSWTQDQS 60  
QY 189 KDSTYSMSSTLTLTCKDEYRHSNTCEATHKTSTSPVKSFNNEC 234  
DB 61 KDSTYSMSSTLTLTCKDEYRHSNTCEATHKTSTSPVKSFNNEC 106

RESULT 3  
KACA\_RAT  
ID KACA\_RAT STANDARD; PRT; 106 AA.  
AC P01836;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain C region, A allele.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DA;  
RX MEDLINE=82082587; PubMed=6273908;  
RA Sheppard H.W., Gutman G.A.;  
RT "Allelic forms of rat kappa chain genes: evidence for strong  
RT selection at the level of nucleotide sequence.";  
RL proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).  
DR PIR: A02118; KIRTA.  
DR HSSP: P01842; 2MCG.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003597; Ig\_cl.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00407; IGcl; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106  
SQ SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;  
Query Match 39.0%; Score 481; DB 1; Length 106;  
Best Local Similarity 84.0%; Pred. No. 4.2e-32;  
Matches 89; Conservative 11; Mismatches 6; Indels 0; Gaps 0;  
QY 129 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQGVLSWTQDQS 188  
DB 1 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQGVLSWTQDQS 60

```
Db 1 ADAAPTIVSIFPPSMEQLTSGGATVVCVFNNFYPRDISVKKWKIDSGEQRDGVLDSTVDQDS 60
QY 189 KDSTYSMSSTLTLPKDEYERHNSYTCETHTKTSPIVKSFNNEC 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 KDSTYSMSSTLTSLTKVEYERHNLXTCEVHHKTSSTSSPVVKSFNNEC 106

RESULT 4
KV5D_MOUSE
ID KV5D_MOUSE STANDARD; PRT; 108 AA.
AC P01636;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 149.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=82057806; PubMed=6795447;
RA Appella E., Alvarez V.L.;
RT "Amino acid sequence of the variable region of M149 mouse myeloma
RT light chain: comparison with the nucleotide sequence of K2 and K3
RT clones."
RL Mol. Immunol. 17:1507-1513(1980).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01919; KVS49.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12030 MW; 0B5244D2B410D84C CRC64;

Query Match 39.0%; Score 481; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 4.3e-32;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASGCVTITCRASGNITQNYLAWYQQTQKSPQLLVYSAKTLADGVPS 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    1 DIQMTQSPDLSASGCVTITCRASENIYSYLAWYQKQKSPQLLVYDAKTLVEGVPS 60

QY 81 RPSGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    61 RPSGSGSGTQFSLKINSLOPEDFGSYCOHHYIPFTFGSGKLEIKR 108

RESULT 5
KACB_RAT
ID KACB_RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=LOU;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes."
RL J. Immunol. 115:59-62(1975).
DR PIR: A02117; K1RTB.
DR HSSP: P01842; 2MCG.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; IGC1; 1.
DR PROSITE: PS00290; IGC_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT CONFLICT 106 106 D -> N (IN REF. 2).
FT CONFLICT 30 30 N -> K (IN REF. 2).
FT CONFLICT 48 48 MISSING (IN REF. 2).
FT CONFLICT 79 79 E -> Q (IN REF. 2).
FT CONFLICT 87 87 E -> Q (IN REF. 2).
FT CONFLICT 98 98 V -> VW (IN REF. 2).
FT CONFLICT 100 100 S -> N (IN REF. 2).
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820DICA36 CRC64;

Query Match 37.8%; Score 466; DB 1; Length 106;
Best Local Similarity 80.2%; Pred. No. 6.6e-31;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 129 ADAAPTIVSIFPPSEQLTSGGAVVCFNNFYPRDKINVKWKIDSGERQGVLSWTQDS 188
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    1 ADAAPTIVSIFPPSTEQLATGASVCLMNNFYPRDISVKKWKIDGTRRDGVLDSTVDQDS 60

QY 189 KDSTYSMSSTLTLPKDEYERHNSYTCETHTKTSPIVKSFNNEC 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    61 KDSTYSMSSTLTSLTKADYESHNLTYTCVHHKTSSTSSPVVKSFNNEC 106

RESULT 6
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
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DR -Pfam; PF00047; ig; 1.  
DR SMART; SM00406; igv; 1.  
KW Immunoglobulin v region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 23 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;  
  
Query Match 35.3%; Score 436; DB 1; Length 129;  
Best Local Similarity 64.6%; Pred. No. 2.le-28;  
Matches 82; Conservative 18; Mismatches 27; Indels 0; Gaps 0;  
  
Qy 1 MSLVQLVALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
Db 3 MRVPAQLLGLLLWLRVRCDIQMTQSPSSLSASVGDVRVITCRAGHNITNFLSWYQKP 62  
  
Qy 61 GKSPQLLVYSAKTLADGVPRFSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGG 120  
Db 63 GKAPLLIYASVLSQGVTSRFSFGSGGTDTFTLTSSLPEDSATYTCQOSYSTLTITFGQ 122  
  
Qy 121 GTKLEIK 127  
Db 123 GTRLEIK 129  
  
RESULT 8  
KV1J\_HUMAN STANDARD; PRT; 117 AA.  
ID KV1J\_HUMAN  
AC P01602;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region HK102 precursor (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=81098966; PubMed=6779204;  
RA Bentley D.L., Rabbitts T.H.;  
RT "Human immunoglobulin variable region genes -- DNA sequences of two V  
RT kappa genes and a pseudogene.";  
RL Nature 288:730-733(1980).  
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CC  
CC EMBL; J00245; AAA59087.1; -  
CC EMBL; Z00001; CAA77292.1; -  
CC PIR; A01882; K1HU12.  
CC HSP; P01607; 1REI.  
CC Genew; HGNC:5741; IGKV1-5.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR003596; Ig\_V.  
CC Pfam; PF00047; ig; 1.  
CC SMART; SM00406; igv; 1.  
KW Immunoglobulin v region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK102.

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C  
R EMBL; X00965; CAA25477.1; ALT\_TERM.  
R PIR; A01883; K1HUW.  
R HSP; P01607; 1REI.  
R InterPro; IPR003006; Ig\_MHC.  
R InterPro; IPR003596; Ig\_V.  
R Pfam; PF00047; ig; 1.  
R SMART; SM00406; igv; 1.  
W Immunoglobulin v region; Signal.  
T SIGNAL 1 22  
T CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
T DOMAIN 23 45 FRAMEWORK-1.  
T DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
T DOMAIN 57 71 FRAMEWORK-2.  
T DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
T DOMAIN 79 110 FRAMEWORK-3.  
T DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
T DOMAIN 120 129 FRAMEWORK-4.  
T DISULFID 45 110 BY SIMILARITY.  
T NON\_TER 129 129  
Q SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;  
  
Query Match 36.7%; Score 453; DB 1; Length 129;  
Best Local Similarity 69.3%; Pred. No. 9.2e-30;  
Matches 88; Conservative 15; Mismatches 24; Indels 0; Gaps 0;  
  
Qy 1 MSLVQLVALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
Db 3 MRVPAQLLGLLLWLRVRCDIQMTQSPSSLSASVGDVRVITCRASQSISNYLWYQKP 62  
  
Qy 61 GKSPQLLVYSAKTLADGVPRFSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGG 120  
Db 63 GKAPLLIYASVLSQGVTSRFSFGSGGTDTFTLTSSLPEDSATYTCQOSYSTLTITFGQ 122  
  
Qy 121 GTKLEIK 127  
Db 123 GTRLEIK 129  
  
RESULT 7  
KV1X\_HUMAN STANDARD; PRT; 129 AA.  
ID KV1X\_HUMAN  
AC P04432;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Daudi precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=85014148; PubMed=6091049;  
RA Klobbeck H.G., Combriato G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
RT lymphoid cell lines are closely related.";  
RL Nucleic Acids Res. 12:6995-7006(1984).  
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CC  
CC EMBL; X00966; CAA25478.1; ALT\_TERM.  
CC PIR; A01884; K1HUI.  
CC HSP; P03362; 1WTL.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR003596; Ig\_V.

```
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 >117
FT DISULFID 45 110
FT NON_TER 117 117
SQ SEQUENCE 117 AA; AD1DF3A40AF1A49B CRC64;

Query Match
Best Local Similarity 33.1%; Score 409; DB 1; Length 117;
Matches 75; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSVLTQVLAALLLWLTGARCIDIQTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQ 60
DB 3 MRVPAQLGLLLWLPFGAKDIQMTQSPSSVSGVDRVITTCRASQSTSSWLAWYQOKP 62
QY 61 GKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPDEFGSYVCOHF 111
DB 63 GKAPKLLIYDASSLESGVPSRFGSGSGTEFTLTISLQPDFAFYCOY 113

RESULT 9
KV5E_MOUSE STANDARD; PRT: 128 AA.
AC P01637;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81052342; PubMed=6776411;
RA Altenburger W., Steinmetz M., Zachau H.G.;
RT "Functional and non-functional joining in immunoglobulin light chain
genes of a mouse myeloma."
RL Nature 287:603-607(1980).
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CC -----
CC EMBL: V00772; CAA24150.1; -
CC PIR: A01920; KYHST1.
CC HSSP: P80362; IWLTL.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig_v.
CC SMART: SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 20
CC CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
CC DOMAIN 21 43 FRAMEWORK-1.
CC DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 69 FRAMEWORK-2.
CC DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 77 108 FRAMEWORK-3.
CC DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 118 127 FRAMEWORK-4.
CC DISULFID 43 108 BY SIMILARITY.
CC NON_TER 128 128
CC SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

Query Match
Best Local Similarity 32.6%; Score 402; DB 1; Length 128;
Matches 75; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
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Best Local Similarity 59.4%; Pred. No. 1.le-25;
Matches 76; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSVLTQVLAALLLWLTGARCIDIQTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQ 60
DB 1 MRPAPQFLGLLLWLPFGIKDKIKMTQSPSSVSGVDRVITTCRASQDINSYLTWFOQKP 60
QY 61 GKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPDEFGSYVCOHFWSPTPTFGG 120
DB 61 GKSPKTLRYRANRLVDGVPDRFGSGSGQDFTLTISLVEDMGIIYCLQYDFEPLTFGA 120
QY 121 GTKLEIKR 128
DB 121 GTKLEIKR 128

RESULT 10
KVLS_HUMAN STANDARD; PRT: 108 AA.
ID KVLS_HUMAN
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092379; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes)."
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01877; KIHUWS.
CC HSSP: P80362; IWLTL.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig_v.
CC SMART: SM00406; IGV; 1.
CC Immunoglobulin V region; Bence-Jones protein.
CC DOMAIN 1 23 FRAMEWORK-1.
CC DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 35 49 FRAMEWORK-2.
CC DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 57 88 FRAMEWORK-3.
CC DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 98 107 FRAMEWORK-4.
CC DISULFID 23 88 BY SIMILARITY.
CC NON_TER 108 108
CC SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match
Best Local Similarity 32.5%; Score 401; DB 1; Length 108;
Matches 74; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQCKSPQLLYVSAKTLADGVPS 80
DB 1 DIQMTQSPSSVSGVDRVITTCRASQDINSYLTWFOQKP 80
QY 81 RFGSGSGTQYSLKINSLOPDEFGSYVCOHFWSPTPTFGGKLEIKR 128
DB 61 RFGSGSGTEFTLTISLQPDFAFYCOQAHVPLTFGGGTTVDIKR 108

RESULT 11
KV1H_HUMAN STANDARD; PRT: 108 AA.
ID KV1H_HUMAN
```

P01600;  
21-JUL-1986 (Rel. 01, Created)  
21-JUL-1986 (Rel. 01, Last sequence update)  
15-JUL-1999 (Rel. 38, Last annotation update)  
Ig kappa chain V-I region Hau.  
E S Homo sapiens (Human).  
S Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE.  
MEDLINE=71032830; PubMed=4097974;  
Watanabe S., Hilschmann N.;  
"The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups";  
Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
PIR; A01868; KIHUHU.  
HSSP; P80362; IWL.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
Immunoglobulin V region; Bence-Jones protein.  
DOMAIN 1 23  
DOMAIN 24 34  
DOMAIN 35 49  
DOMAIN 50 56  
DOMAIN 57 88  
DOMAIN 89 97  
DOMAIN 98 107  
DOMAIN 108 108  
DISULFID 23 88  
NON\_TER 108 108  
SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;  
Query Match 32.3%; Score 399; DB 1; Length 108;  
Best Local Similarity 68.5%; Pred. No. 1.6e-25;  
Matches 74; Conservative 18; Mismatches 16; Indels 0; Gaps 0;  
21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQKSPQLLYVSAKTLDGVPS 80  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 DIQMTQSPSSLSASVGDRTVTITCRASGSISSYLSWYQKPKAPQVLIYAASLPSGVPS 60  
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKR 128  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 RFGSGSGTDFLTLSISLQPEDFATYQCQYNYITPTSGGCTRVEIKR 108  
RESULT 12  
KV10\_HUMAN  
ID KV10\_HUMAN STANDARD; PRT; 108 AA.  
AC P01595;  
OT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region BI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=73029807; PubMed=4563064;  
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;  
"Principle of antibody structure. The primary structure of a monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein BI). 3. The complete amino acid sequence and the genetic significance of the variability principles for the mechanism of antibody formation";  
Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).  
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
PIR; A01863; KIHUBI.  
HSSP; P01607; IREI.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
Immunoglobulin V region; Bence-Jones protein.  
DOMAIN 1 23  
DOMAIN 24 34  
DOMAIN 35 49  
DOMAIN 50 56  
DOMAIN 57 88  
DOMAIN 89 97  
DOMAIN 98 107  
DOMAIN 108 108  
DISULFID 23 88  
NON\_TER 108 108  
SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;  
Query Match 32.1%; Score 396; DB 1; Length 108;  
Best Local Similarity 67.6%; Pred. No. 2.7e-25;  
Matches 73; Conservative 17; Mismatches 18; Indels 0; Gaps 0;  
21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQKSPQLLYVSAKTLDGVPS 80  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 DIQMTQSPSSLSASVGDSTVTITCASQSDIRNSLIWYQKPKAPKFLIYDAENLEIGVPS 60  
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKR 128  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 RFGSGSGTDFALSISLQPEDFATYQCQYNYITPTFGGCTKLEIKR 108  
RESULT 13  
KV10\_HUMAN  
ID KV10\_HUMAN STANDARD; PRT; 108 AA.  
AC P01607;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Rel.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76023758; PubMed=8093329;  
RA Palm W., Hilschmann N.;  
"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site";  
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
[2]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=76039968; PubMed=1182131;  
RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;  
"The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rel refined at 2.0-A resolution.";  
Biochemistry 14:4943-4952(1975).  
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
PIR; A01873; KIHURE.  
PDB; IREI; 17-FEB-84.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
DOMAIN 1 23  
FRAMEWORK-1.



```
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT FT 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT FT 107 107 FRAMEWORK-4.
FT FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 98E143E1188BCE2A CRC64;

Query Match 32.0%; Score 395; DB 1; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.2e-25;
Matches 75; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITTCRASGNIGNYLAWYQQTQKSPQLLYVYSAKTLADGVPS 80
Db 1 DIQMTQSPSSLSASVGDVRVITTCRASQSDIIKYNWYQQTQKAPKLLIYEASNLQAGVPS 60
QY 81 RFGSGSGTQYSLKINSLOPEDFGSGYCOHFWSPTPTFGGKLEIKR 128
Db 61 RFGSGSGTDITFTISSLPEDIATYYCOYQSLPYTFGGTKLIQTR 108

RESULT 14
KV1L_HUMAN STANDARD; PRT; 108 AA.
ID KV1L_HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHU11.
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Amyloid.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT FT 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
```

```
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 31.8%; Score 392; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 5.6e-25;
Matches 72; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITTCRASGNIGNYLAWYQQTQKSPQLLYVYSAKTLADGVPS 80
Db 1 DIQMTQSPSSLSASVGDVRVITTCRASQSVYVAVFWFQKPKRPSLIYDASTLQSGVPS 60
QY 81 RFGSGSGTQYSLKINSLOPEDFGSGYCOHFWSPTPTFGGKLEIKR 128
Db 61 NFGSGSGTDFILITISSLPEDFATYYCOYNSPYTFGGTKVQIKR 108

RESULT 15
KV1L_HUMAN STANDARD; PRT; 117 AA.
ID KV1L_HUMAN
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion.";
RL Cell 32:181-189(1983).
CC -----
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CC -----
DR EMBL; K01322; AAA58930.1; -
DR EMBL; K01324; AAA58932.1; -
DR EMBL; V00558; CAA23824.1; -
DR PIR; A01881; KIHU11.
DR PIR; A21056; A21056.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 17.0899 Seconds  
(without alignments)  
1316.302 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVLALLLLWLTGARG.....EATHKTSPIVKSFRNREC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pirl:\*

2: pirl2:\*

3: pirl3:\*

4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1127	91.3	234	2 S01320	Ig kappa chain pre
2	966	78.3	234	2 S14237	Ig kappa chain pre
3	898	72.8	220	2 A13790	Ig kappa chain pre
4	892.5	72.3	235	2 S25058	Ig kappa chain - m
5	889.5	72.1	225	2 S37484	Ig kappa chain - m
6	887	71.9	214	2 S68212	Ig kappa chain (Ma
7	876	71.0	218	2 JC5810	monoclonal antibod
8	868	70.3	218	2 S68241	Ig kappa chain v r
9	867.5	70.3	219	2 PC4203	Ig kappa chain (mo
10	864.5	70.1	219	2 S52028	Ig kappa chain - m
11	863	69.9	240	2 S05084	Ig kappa chain pre
12	862.5	69.9	219	2 S38865	Ig kappa chain - m
13	860.5	69.7	219	2 S16112	Ig kappa chain v r
14	854.5	69.2	225	2 JL0029	Ig kappa chain pre
15	851.5	69.0	217	2 S42772	Ig kappa chain - m
16	849	68.8	210	2 A56169	Ig kappa chain v r
17	744.5	60.3	230	2 S33161	Ig kappa chain - s
18	704.5	57.1	197	2 S29593	Ig kappa chain (WM
19	689.5	55.9	215	2 JE0244	Ig kappa chain NIG
20	685.5	55.6	215	2 JE0242	Ig kappa chain NIG
21	669.5	54.3	215	2 JE0243	Ig kappa chain NIG
22	642.5	52.1	215	2 A23746	Ig kappa chain V-I
23	639.5	51.8	229	2 A20969	Ig kappa chain pre
24	612	49.6	216	2 JE0241	Ig kappa chain pre
25	592	48.0	128	2 S31488	Ig kappa chain An3
26	586	47.5	115	1 KWSK2	Ig kappa chain pre
27	579	46.9	134	2 S11245	Ig kappa chain pre
28	578	46.8	178	2 P01219	Ig kappa chain v-c
29	570	46.2	126	2 I54782	gene Pvt-1a/Ig-Ck

#### ALIGNMENTS

##### RESULT 1

S01320

Ig kappa chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 21-Jan-2000

C:Accession: S01320

R:de Waele, P.; Feys, V.; van de Voorde, A.; Mollemans, F.; Fiers, W.

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe

A:Reference number: S01320; MUID:88329081; PMID:3138116

A:Accession: S01320

A:Molecule type: mRNA

A:Residues: 1-234 <DEL>

A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785

A:Note: This sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-234/Product: Ig kappa chain #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 91.3%; Score 1127; DB 2; Length 234;

Matches 215; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSVLTVLALLLLWLTGARGDIQMTSPASISASVGETVITTCRASGNIONYLAWYQQTQ 60

Db. 1 MSVPTQVLGLLLWLTGARGDIQMTSPASISVSVGESVITTCRASNIYSLNLAWYQKQ 60

QY 61 GKSPQLLVYSAKTLADGVPSRFSGSGSTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 120

Db 61 GKSPQLLVYVATKLVDPVPSRFSGSGSTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 120

QY 121 GTKLETKRADAAPTIVIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSGRQNGVL 180

Db 121 GTKLEMKRADAAPTIVIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSGRQNGVL 180

QY 181 NSWTDODSKDTSYMSSTLTITKDEYERHNSYTCETHKTSSTSPIVKSFNRNRC 234

Db 181 NSWTDODSKDTSYMSSTLTITKDEYERHNSYTCETHKTSSTSPIVKSFNRNRC 234

##### RESULT 2

S14237

Ig kappa chain precursor (15C5) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C:Accession: S14237

R.Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Eur. J. Biochem. 192, 767-775, 1990

A:Title: Construction and characterization of a recombinant murine monoclonal antibod

A:Reference number: S14236; MUID:91006173; PMID:2209622

C:Accession: S25058  
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi  
 A:Reference number: S25057  
 A:Accession: S25058  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <FIS>  
 A:Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 892.5; DB 2; Length 235;  
 Best Local Similarity 73.3%; Pred. No. 1.5e-48;  
 Matches 173; Conservative 19; Mismatches 41; Indels 3; Gaps 2;

QY 1 MSVLTQVLALLLWLTG--ARCDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQ 58  
 Db 1 MDTQVQLFSLLLSASVILSRGQIVLTQSPAIMSASPEKVTWTCSSASSVSK-MQWYQQ 59

QY 59 TQKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTTF 118  
 Db 60 KSGTSPKRWIYDTSKLASGVPSRFGSGSGTQYSLTSSMEADAATYCCQWSSNPLTF 119

QY 119 GGKTKLEIKRADAAPTIVSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNG 178  
 Db 120 GAGTKLEIKRADAAPTIVSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNG 179

QY 179 VLNSWTDQDSDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234  
 Db 180 VLNSWTDQDSDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 235

RESULT 5

S37484  
 Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000  
 C:Accession: S37484  
 R:Ducancel, F.F.D.  
 submitted to the EMBL Data Library, February 1993  
 A:Reference number: S37483  
 A:Accession: S37484  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-225 <DUC>  
 A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 72.1%; Score 889.5; DB 2; Length 225;  
 Best Local Similarity 75.9%; Pred. No. 2.1e-48;  
 Matches 170; Conservative 21; Mismatches 32; Indels 1; Gaps 1;

QY 11 LLLWLTGARCIDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTKGSPQLLYVS 70  
 Db 3 LLLCVSGAHGSIIVMTQPKFLLSAGDRVTTCRASQSVNDVAVYQKPGSPKLLIY 62

QY 71 AKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKTKLEIKRAD 130  
 Db 63 ASSRYTGVDPDRFTGSGYCTDFTTISTVQAEADLAVYFCQDYSS-YTFGGGTGLEIKRAD 121

QY 131 AAPTIVSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSD 190  
 Db 122 AAPTIVSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSD 181

QY 191 STYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234  
 Db 182 STYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 225

RESULT 6

C:Accession: S14237  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <VAN>  
 A:Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 966; DB 2; Length 234;  
 Best Local Similarity 77.8%; Pred. No. 4.2e-53;  
 Matches 182; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

Y 1 MSVLTQVLALLLWLTGARCIDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQ 60  
 b 1 MRTPAQFLGILLWFFGIKDIKMTQSPSSMYASLGERVTVTCKASQDINSYLSWQQKP 60

Y 61 GKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 120  
 b 61 GKSPKTLIYRGNRLVAGVPSRFGSGSGTQYSLTSSLEYEDGVYCYCLRYDEFFTFGS 120

Y 121 GTKLEIKRADAAPTIVSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 180  
 b 121 GTKLEIKRADAAPTIVSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 180

Y 181 NSWTDQDSDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234  
 b 181 NSWTDQDSDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234

RESULT 3

S31790  
 g kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
 C:Accession: A31790  
 C:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
 J. Biol. Chem. 263, 17100-17105, 1988  
 A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an  
 A:Reference number: A92686; MUID:89034213; PMID:3182835  
 A:Accession: A31790  
 A:Molecule type: mRNA  
 A:Residues: 1-220 <SCH>  
 A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 898; DB 2; Length 220;  
 Best Local Similarity 76.8%; Pred. No. 6.3e-49;  
 Matches 169; Conservative 19; Mismatches 26; Indels 6; Gaps 1;

Y 21 DIQMTQSPASLSASVGETVITTCRA-----SGNIQNYLAWYQQTKGSPQLLYVSAKTL 74  
 Db 1 DIVMTQSPSSLTIVTAGEKVTMSTSSQSLFNSGKQKYLWYQKPGPKVLIYWASTR 60

Y 75 ADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKTKLEIKRADAAPT 134  
 Db 61 ESGVDPDRFTGSGSGTDFLTITSSVQAEADLAVYQNDYSNPLTFGGGTGLEIKRADAAPT 120

Y 135 VSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSDSTYS 194  
 Db 121 VSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSDSTYS 180

Y 195 MSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234  
 Db 181 MSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 220

RESULT 4

S25058  
 Ig kappa chain - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000

S68212		Ig kappa chain (Mab03-1) - mouse (fragment)	
C:Species: Mus musculus (house mouse)		N;Alternate names: immunoglobulin light chain	
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000		C:Accession: S68212	
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.		FBS Lett. 375, 273-276, 1995	
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin		A:Reference number: S68211; MUID:96085223; PMID:7498516	
A:Accession: S68212		A:Status: preliminary; nucleic acid sequence not shown	
A:Molecule type: mRNA		A:Residues: 1-214 <TAK>	
A:Cross-references: EMBL:D29668		A:Superfamily: immunoglobulin V region; immunoglobulin homology	
Query Match		71.9%; Score 887; DB 2; Length 214;	
Best Local Similarity		79.0%; Pred. No. 2.9e-48;	
Matches 169; Conservative 17; Mismatches 22; Indels 6; Gaps 1;			
QY	21	DIQMTQSPASLSASVGETVTITCR-----SGNIQNYLAWYQQTQKSPQLLYVSAKTL 74	
Db	1	DIQMTQSPASLSASVGETVTITCR-----SGNIQNYLAWYQQTQKSPQLLYVSAKTL 74	
QY	75	ADGVPSRFSGSGGTQYSLKINSIQPEDFGSYVCOHFWSTPTTFGGGKLEIKRADAAPT 134	
Db	61	ESGVPDFRFGSGGTDFLTITSTVQADLADYFCQHYSTPTTFGGGKLEIKRADAAPT 120	
QY	135	VSIFPPSSEQLTSGGAVVCFNNFYPKIDINVKWKIDGSRQNGVLSWTDQDSKSTYS 194	
Db	121	VSIFPPSSEQLTSGGAVVCFNNFYPKIDINVKWKIDGSRQNGVLSWTDQDSKSTYS 180	
QY	195	MSSTLTLTQDEYERHNSYTCETHKTSPIVKS 228	
Db	181	MSSTLTLTQDEYERHNSYTCETHKTSPIVKS 214	
RESULT 7		Query Match	
JC5810		70.3%; Score 868; DB 2; Length 218;	
monoclonal antibody 13-1 light chain - mouse		Best Local Similarity 74.8%; Pred. No. 4.4e-47;	
C:Species: Mus musculus (house mouse)		Matches 163; Conservative 21; Mismatches 30; Indels 4; Gaps 1;	
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000			
C:Accession: JC5810			
R:Kashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.			
Biochem. Biophys. Res. Commun. 240, 566-572, 1997			
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin			
A:Reference number: JC5810; MUID:98063277; PMID:9398605			
A:Accession: JC5810			
A:Molecule type: protein			
A:Residues: 1-218 <AKA>			
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
F:16-94/Domain: immunoglobulin homology <IMX>			
Query Match		71.0%; Score 876; DB 2; Length 218;	
Best Local Similarity 75.7%; Pred. No. 1.4e-47;			
Matches 165; Conservative 20; Mismatches 29; Indels 4; Gaps 1;			
QY	21	DIQMTQSPASLSASVGETVTITCRASGNIQN-----YLAWYQQTQKSPQLLYVSAKTLAD 76	
Db	1	NIYLTQSPASLSASVGETVTITCRASGNIQN-----YLAWYQQTQKSPQLLYVSAKTLAD 76	
QY	77	GVPSRFSGSGGTQYSLKINSIQPEDFGSYVCOHFWSTPTTFGGGKLEIKRADAAPT 136	
Db	61	GVPSRFSGSGGTQYSLKINSIQPEDFGSYVCOHFWSTPTTFGGGKLEIKRADAAPT 120	
QY	137	IFPPSSEQLTSGGAVVCFNNFYPKIDINVKWKIDGSRQNGVLSWTDQDSKSTYSMS 196	
Db	121	IFPPSSEQLTSGGAVVCFNNFYPKIDINVKWKIDGSRQNGVLSWTDQDSKSTYSMS 180	
QY	197	STLTLTQDEYERHNSYTCETHKTSPIVKSFNREC 234	
Db	181	STLTLTQDEYERHNSYTCETHKTSPIVKSFNREC 218	
RESULT 9		Query Match	
PC4203		70.3%; Score 867.5; DB 2; Length 219;	
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)		Best Local Similarity 75.3%; Pred. No. 4.8e-47;	
C:Species: Mus musculus (house mouse)		Matches 165; Conservative 16; Mismatches 33; Indels 5; Gaps 1;	
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000			
C:Accession: PC4203			
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.			
Gene 173, 257-259, 1996			
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a			
A:Reference number: PC4202; MUID:97082978; PMID:8964510			
A:Accession: PC4203			
A:Molecule type: mRNA			
A:Residues: 1-219 <KWA>			
A:Cross-references: GB:U29147; NID:gi1594225; PIDN:AAC52821.1; PID:gi1594226			
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-densi			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
F:1-112/Domain: V region #status predicted <VRG>			
F:113-219/Domain: C region #status predicted <CRG>			
Query Match		70.3%; Score 867.5; DB 2; Length 219;	
Best Local Similarity 75.3%; Pred. No. 4.8e-47;			
Matches 165; Conservative 16; Mismatches 33; Indels 5; Gaps 1;			

21 DIQWTSQSPASLSASVGETVITICRAGNI-----QNYLAWYQQTQKSPQLLYVSAKTLA 75  
1 DVLMTQTPSLVSLGDAQSISCRSSQIVHTNGNTYLEWYLPKQSPKLLIYKVSNR 60  
76 DGVPSRFRSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTPKLEIKRADAAPT 135  
61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGGSHVPTFGGTPKLEIKRADAAPT 120  
136 SIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 195  
121 SIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180  
196 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 234  
181 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 219  
RESULT 10  
S52028  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S52028  
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;  
submitted to the EMBL Data Library, August 1994  
A:Description: Coordinate expression of antibody subunit genes yields high levels of fun  
A:Reference number: S52028  
A:Accession: S52028  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <V>  
A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
A:Keywords: heterotetramer; immunoglobulin  
A:Domain: immunoglobulin homology <IMM>  
Query Match 70.1%; Score 864.5; DB 2; Length 219;  
Best Local Similarity 75.3%; Pred. No. 7.3e-47;  
Matches 165; Conservative 15; Mismatches 34; Indels 5; Gaps 1;  
21 DIQWTSQSPASLSASVGETVITICRAGNI-----QNYLAWYQQTQKSPQLLYVSAKTLA 75  
1 DVLMTQTPSLVSLGDAQSISCRSSQIVHTNGNTYLEWYLPKQSPKLLIYKVSNR 60  
76 DGVPSRFRSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTPKLEIKRADAAPT 135  
61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGGSHVPTFGGTPKLEIKRADAAPT 120  
136 SIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 195  
121 SIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180  
196 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 234  
181 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 219  
RESULT 11  
S06084  
Ig kappa chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S06084  
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A:Title: Nucleotide sequence of V3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA  
A:Reference number: S06084; MUID:90016888; PMID:2508067  
A:Accession: S06084  
A:Molecule type: mRNA  
A:Residues: 1-240 <C>  
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
A:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-240/Product: Ig kappa chain #status predicted <MAT>  
F:153-222/Domain: immunoglobulin homology <IMM>  
Query Match 69.9%; Score 863; DB 2; Length 240;  
Best Local Similarity 67.5%; Pred. No. 9.9e-47;  
Matches 162; Conservative 31; Mismatches 41; Indels 6; Gaps 1;  
QY 1 MSVLTVQVLAALLLWLTGARDIQMTQSPASLSASVGETVITICRA-----SGNIONYLA 54  
DB 1 MESQTVLMSLLWISGTCGDFVMTQSPSLAVSAGETVITINCKSSQSLFYSGNQKNYLA 60  
QY 55 WYQQTQKSPQLLYVSAKTLADGVPSRFRSGSGGTQYSLKINSLOPEDFGSYCOHFWSPT 114  
DB 61 WYQQTQKSPQLLYVSAKTLADGVPSRFRSGSGGTQYSLKINSLOPEDFGSYCOHFWSPT 120  
QY 115 PYTFGGTGTLEIKRADAAPTIVSIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSE 174  
DB 121 PYTFGGTGTLEIKRADAAPTIVSIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSE 180  
QY 175 RQGVLSNWTQDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 234  
DB 181 RQGVLSNWTQDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 240  
RESULT 12  
S38865  
Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
C:Accession: S38865  
R:Kipp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of  
A:Reference number: S38864  
A:Accession: S38865  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <KIP>  
A:Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
A:Keywords: heterotetramer; immunoglobulin  
Query Match 69.9%; Score 862.5; DB 2; Length 219;  
Best Local Similarity 74.4%; Pred. No. 9.7e-47;  
Matches 163; Conservative 18; Mismatches 33; Indels 5; Gaps 1;  
QY 21 DIQWTSQSPASLSASVGETVITICRAGNI-----QNYLAWYQQTQKSPQLLYVSAKTLA 75  
DB 1 ELVMTQSPSLVSLGDAQSISCRSSQIVHTNGNTYLEWYLPKQSPKLLIYVSNRF 60  
QY 76 DGVPSRFRSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTPKLEIKRADAAPT 135  
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGGSHVPTFGGTPKLEIKRADAAPT 120  
QY 136 SIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 195  
DB 121 SIFFPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180  
QY 196 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 234  
DB 181 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNREC 219  
RESULT 13  
S16112  
Ig kappa chain V region (G2a) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S16112  
R:Vaessen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D  
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991  
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp

A:Reference number: S16112; MUID:92000313; PMID:1910583  
A:Accession: S16112  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-219 <BIT>  
C:Superfamily: immunoglobulin V region; immunoglobulin F  
C:Keywords: heterotetramer; immunoglobulin  
F16-95/Domain; immunoglobulin homology <IMM>

Query Match	69.7%	Score	860.5	DB 2	Length	219																						
Best Local Similarity	74.4%	Pred. No.	1.3e-46																									
Matches	163	Conservative	17	Mismatches	34	Indels	5	Gaps	1																			
QY	21	DIQMTQSPASLSASVGETVTITCRAS----	GNIQNYLAWYQOTQGSQPOLLYVS	SAKTLA	75																							
Db	1	DVVMQTPLSLPVSLGDQASISCRSSQSLVHSG	NGNTYLIIWLOKPGQSPKPLIYRVS	NRF	60																							
QY	76	DGVPSRFSGS	GGTQYSLKINS	LPD	FGSYCQHF	WSTPT	YTFGGG	T	KLEIKR	ADAAPTV	135																	
Db	61	SGVPSRFSGS	GGTDFTLKIS	VEAEDL	GVYFC	FQGT	HYPT	YTFGGG	T	KLEIKR	ADAAPTV	120																
QY	136	SIFPPSS	SEQLTSGGASV	VCFLN	FPK	DLN	VKWK	IDG	S	ERQNGV	LN	SWTD	DQD	SKD	STYS	M	195											
Db	121	SIFPPSS	SEQLTSGGASV	VCFLN	FPK	DLN	VKWK	IDG	S	ERQNGV	LN	SWTD	DQD	SKD	STYS	M	180											
QY	196	SSTLT	LT	TD	EY	RHNS	Y	CE	A	T	H	K	T	S	T	S	P	I	V	K	S	F	N	R	N	E	C	234
Db	181	SSTLT	LT	TD	EY	RHNS	Y	CE	A	T	H	K	T	S	T	S	P	I	V	K	S	F	N	R	N	E	C	219

```

RESULT 14
JL0029
;;Title: Ig kappa chain precursor (RP93) - mouse (fragment)
;;Species: Mus musculus (house mouse)
;;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
;;Accession: JL0029
;;Author: Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
;;J. Exp. Med. 167, 954-973, 1988
;;Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor
;;Reference number: JL0029; MUID:88171315; PMID:3127529
;;Accession: JL0029
;;Molecule type: mRNA
;;Residues: 1-225 <CHI>
;;Experimental source: strain BALB/c, cell line RP93 hybridoma cell
;;Note: The authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
;;Note: the nucleotide sequence shown is inconsistent with authors' translation because
;;Comment: The protein is an anti-phosphorylcholine antibody.
;;Superfamily: immunoglobulin V region; immunoglobulin homology
;;Keywords: immunoglobulin
;;7-225/Product: Ig kappa chain #status predicted <ILC>
;;7-106/Domain: V region #status predicted <VAR>
;;107-119/Domain: J region #status predicted <JIR>
;;120-225/Domain: C region #status predicted <COR>

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Query Match	69.2%;	Score 854.5;	DB 2;	Length 225;
Best Local Similarity	74.4%;	Pred. No. 3.1e-46;		
Matches 163;	Conservative 15;	Mismatches 36;	Indels 5;	Gaps 1;
Y	21	DIQMTCSPASLASASGVEFVTTTCRASGNI-----QNYLAWYQQTGGKSPQLLVYSAKTLA	75	
b	7	DIWLTQIPULSPVSLGDQASISCRSQNVHSTGNTYLEWYLQKPGQSPNLLIYKISNRF	66	
Y	76	DGVPGRFSGSGSGTQYSLKINSIQLOPEDRGSVYCOHFNPTPYTFGGGKYLEIKRADAAPT	135	
b	67	SGVPDRFSGSGSGTDFSLGISRVEAEDLGVIYCFQSSHVRRWTFGGGKYLEIKRADAAPT	126	
Y	136	SIFPPSSEQLTSGGASVVCFLNNFPKDIYKWKIDGSENGVINSWTDQDSKDSYISM	195	
b	127	SIFPPTSEQLTSGGASVVCFLNNFPKDIYKWKIDGSENGVINSWTDQDSKDSYISM	186	
Y	196	STTLPLTKDEYERHNSYTCEATHKTIPTSPYIKSFNRNEC	234	

Db 187 SSTLTLTKDEYERHNSYTCEATHNTSTSPIVKSFRNEC 225

## RESULT 15

S42772	<p>Ig kappa chain - mouse</p> <p>C:Species: Mus musculus (house mouse)</p> <p>C:Date: 06-Jan-1995 #sequence_revision</p> <p>C:Accession: S42772</p> <p>R:Schellekens, G.A.</p> <p>submitted to the EMBL Data Library, November 1993</p> <p>A:Reference number: S42771</p> <p>A:Accession: S42772</p> <p>A:Status: preliminary</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-217 &lt;SCH&gt;</p> <p>A:Cross-references: EMBL:X75536; NID:g414143; PIDN:CRAA53226.1; PID:g414144</p> <p>C:Superfamily: immunoglobulin V region; immunoglobulin homology</p> <p>C:Keywords: heterotetramer; immunoglobulin</p> <p>F:14-93/Domain: immunoglobulin homology &lt;IMM&gt;</p>
--------	--

[illegible]

Search completed: June 18, 2003, 16:47:05  
Job time : 18.0899 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 27.6067 Seconds  
(without alignments)  
2164.388 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVLALLLEWLTGARC.....EATHKTSPIVKSFNNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1156168 seqs, 255349102 residues

Total number of hits satisfying chosen parameters: 1156168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA.New:\*

- 1: /cgn2\_6/ptodata/2/paa/PTCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	985	79.8	237	6	US-10-219-051B-3411
2	985	79.8	237	6	US-10-219-051B-12786
3	985	79.8	237	6	US-10-219-051B-14374
4	918	74.4	238	6	US-10-384-933-11
5	907	73.5	211	6	US-10-236-051-8
6	881.5	71.4	234	1	PTCT-US02-34420A-24
7	881.5	71.4	234	1	PTCT-US02-35333A-24
8	881.5	71.4	234	6	US-10-286-132A-24
9	881.5	71.4	234	6	US-10-281-479A-24
10	881.5	71.4	234	6	US-10-275-180A-24
11	881	71.4	236	5	US-09-726-219A-188
12	845	68.5	215	6	US-10-236-051-4
13	830.5	67.3	216	5	US-09-254-180C-132
14	830.5	67.3	216	5	US-09-254-180C-183
15	818.5	66.3	216	5	US-09-254-180C-182
16	806	65.3	234	1	PTCT-US02-36107-24
17	806	65.3	234	6	US-10-292-088-24
18	806	65.3	237	1	PTCT-US02-22011-109
19	806	65.3	237	6	US-10-194-975-109
20	804	65.2	234	1	PTCT-US02-36107-48
21	804	65.2	234	6	US-10-292-088-48
22	804	65.2	241	1	PTCT-US03-01096-313
23	803	65.1	236	1	PTCT-US03-09260-4
24	803	65.1	236	6	US-10-401-344-4
25	771	62.5	214	5	US-09-618-380A-5
26	766.5	62.1	239	6	US-10-219-051B-12711

27 762 61.8 233 1 PCT-US03-10154-68 Sequence 68, Appl  
28 762 61.8 233 6 US-10-404-724-68 Sequence 68, Appl  
29 761 61.7 4852 6 US-10-412-406-33 Sequence 33, Appl  
30 759 61.5 663 6 US-10-412-406-32 Sequence 32, Appl  
31 756.5 61.3 235 6 US-10-405-027-3083 Sequence 3083, Ap  
32 756.5 61.3 235 6 US-10-405-027-4346 Sequence 4346, Ap  
33 754 61.1 237 1 PCT-US02-27220-4 Sequence 1, Appl  
34 754 61.1 237 6 US-10-1227-694-4 Sequence 1, Appl  
35 751 60.9 237 1 PCT-US02-27220-1 Sequence 1, Appl  
36 751 60.9 237 5 US-09-1724-868-10 Sequence 10, Appl  
37 751 60.9 237 6 US-10-227-694-1 Sequence 1, Appl  
38 751 60.9 237 6 US-10-1234-671-100 Sequence 1, Appl  
39 749 60.7 212 1 PCT-US02-40227A-77 Sequence 100, App  
40 749 60.7 212 6 US-10-320-231A-77 Sequence 77, Appl  
41 748 60.6 214 1 PCT-US03-13054-3 Sequence 3, Appl  
42 748 60.6 214 6 US-10-423-299-3 Sequence 3, Appl  
43 746 60.5 222 6 US-10-424-599-208511 Sequence 208511,  
44 744 60.3 214 5 US-09-1724-868-2 Sequence 2, Appl  
45 744 60.3 214 6 US-10-404-286-11 Sequence 11, Appl

#### ALIGNMENTS

RESULT 1  
US-10-219-051B-3411  
; Sequence 3411, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219,051B  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3411  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; LOCATION: (1)..(237)  
; OTHER INFORMATION: Xaa=Unknown amino acid  
US-10-219-051B-3411  
Query Match 79.8%; Score 985; DB 6; Length 237;  
Best Local Similarity 79.8%; Pred. No. 2.3e-78;  
Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;  
QY 1 MSVLTVLALLLEWLTGARCIDMTQSPASLSASVGETVTITCRASGNIONYLAWTQQTQ 60  
Db 3 MRPAPFLGILLWFFGCMKDIKWTQSPSSMYASLGERVTITCKASODINSYLSWFOQKP 62  
QY 61 GKSPQLLVYSAKTLADGVPSRFSGSGSGGYQYSLKINSLOPEDFGSYVQCFWSTPYTFGG 120  
Db 63 GKSPKTLIYRANRLVDGVPSRFSGSGSGGQDYSLTISSEYEDMGIIYCYLOYDEFPPTFGG 122  
QY 121 GYKLETKRADAPTIVSIFPPPSSEQLTSGGASVVCVFLNNFYPKDINVKWKIDGSEKONGVL 180  
Db 123 GYKLETKRADAPTIVSIFPPPSSEQLTSGGASVVCVFLNNFYPKDINVKWKIDGSEKONGVL 182  
QY 181 NSWTQDSDKSTYSMSSTLTLTAKDEYERHNSYTCETHKTSPTSPVKSFNNEC 234  
Db 183 NSWTQDSDKSTYSMSSTLTLTAKDEYERHNSYTCETHKTSPTSPVKSFNNEC 236

```

RESULT 2
S-10-219-051B-12786
Sequence 12786, Application US/10219051B
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: Lea 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 12786
LENGTH: 237
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(237)
OTHER INFORMATION: Xaa=Unknown amino acid
US-10-219-051B-12786

Query Match 79.8%; Score 985; DB 6; Length 237;
Best Local Similarity 79.5%; Pred. No. 2.3e-78;
Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLWLTGACDIQMTQSPASLSASVGETVITTCRAGNIONYLAWYQQTQ 60
3 MRTPAQFLGILLWFFGKMDIKMTQSPSSMYASLGERTVITCKASODINSYLSWFOQKP 62
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 120
63 GKSPKTLIYRANRLVDGVPSRFGSGSGQDYSLTISSEYEDMGIIYCYLQYDEFPRTFGG 122
121 GTKLEIKRADAAPTSTVIFPPSSSEQLTSGGASVVCFLNNFYPKDNVKKIDGSRQNGVL 180
123 GTKLEIKRADAAPTSTVIFPPSSSEQLTSGGASVVCFLNNFYPKDNVKKIDGSRQNGVL 182
181 NSWTDQSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
183 NSWTDQSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 236

```

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RESULT 3
S-10-219-051B-14374
Sequence 14374, Application US/10219051B
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: Lea 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 14374
LENGTH: 237
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

```

```

; LOCATION: (1)..(237)
; OTHER INFORMATION: Xaa=Unknown amino acid
US-10-219-051B-14374

Query Match 79.8%; Score 985; DB 6; Length 237;
Best Local Similarity 79.5%; Pred. No. 2.3e-78;
Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLWLTGACDIQMTQSPASLSASVGETVITTCRAGNIONYLAWYQQTQ 60
3 MRTPAQFLGILLWFFGKMDIKMTQSPSSMYASLGERTVITCKASODINSYLSWFOQKP 62
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 120
63 GKSPKTLIYRANRLVDGVPSRFGSGSGQDYSLTISSEYEDMGIIYCYLQYDEFPRTFGG 122
121 GTKLEIKRADAAPTSTVIFPPSSSEQLTSGGASVVCFLNNFYPKDNVKKIDGSRQNGVL 180
123 GTKLEIKRADAAPTSTVIFPPSSSEQLTSGGASVVCFLNNFYPKDNVKKIDGSRQNGVL 182
181 NSWTDQSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
183 NSWTDQSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 236

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RESULT 4
US-10-384-933-11
Sequence 11, Application US/10384933
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Ikuko
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
LENGTH: 238
TYPE: PRF
ORGANISM: Mus musculus
US-10-384-933-11

Query Match 74.4%; Score 918; DB 6; Length 238;
Best Local Similarity 72.3%; Pred. No. 1.7e-72;
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

1 MSVLTQVLAALLLLWLTGACDIQMTQSPASLSASVGETVITTCRAGNIONYLAWY 56
1 METDTILLWVWMLIPGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 60
57 QOTGKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPT 116
61 QOKPGQPPKLLIYRANRLVDGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPT 120
117 TFGGKTKLEIKRADAAPTSTVIFPPSSSEQLTSGGASVVCFLNNFYPKDNVKKIDGSRQ 176
121 TFGGKTKLEIKRADAAPTSTVIFPPSSSEQLTSGGASVVCFLNNFYPKDNVKKIDGSRQ 180
177 NGVLSNWTQDQSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
181 NGVLSNWTQDQSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238

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RESULT 5
US-10-236-051-8
; Sequence 8, Application US/10236051

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63 QSPKLLIYWASTRHGTGVPDRFTGSGSGTDFLTITSNVQSEDLADYFCQY-SSYRTFGG 121  
122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181  
122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181  
182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234  
182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234

## RESULT 8

US-10-286-132A-24  
; Sequence 24, Application US/10286132A  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Tong  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: LoBuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.002907  
; CURRENT APPLICATION NUMBER: US/10/286.132A  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct  
US-10-286-132A-24

Query Match 71.4%; Score 881.5; DB 6; Length 234;  
Best Local Similarity 73.4%; Pred. No. 2.7e-69;  
Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

2 SVLTQVALLLMLTGCARDIQMTQSPASLSASVGETVITCRASGNIGNYLAWYQQTGG 61  
3 SLYLVLYTHYLFAGVGGDIWMTQSHKFMSTSVGDRVSIITCKASQDVCTAVAWYQKPG 62  
62 KSPQLLVYSAKTADGVPSRSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 121  
63 QSPKLLIYWASTRHGTGVPDRFTGSGSGTDFLTITSNVQSEDLADYFCQY-SSYRTFGG 121  
122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181  
122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181  
182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234  
182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234

## RESULT 9

US-10-281-479A-24  
; Sequence 24, Application US/10281479A  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: Oshumi, Jun  
; APPLICANT: LoBuglio, Albert S.

; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS  
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T  
; TITLE OF INVENTION: AGENTS  
; FILE REFERENCE: 21085.002906  
; CURRENT APPLICATION NUMBER: US/10/281,479A  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/391,478  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct  
US-10-281-479A-24

Query Match 71.4%; Score 881.5; DB 6; Length 234;  
Best Local Similarity 73.4%; Pred. No. 2.7e-69;  
Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

2 SVLTQVALLLMLTGCARDIQMTQSPASLSASVGETVITCRASGNIGNYLAWYQQTGG 61  
3 SLYLVLYTHYLFAGVGGDIWMTQSHKFMSTSVGDRVSIITCKASQDVCTAVAWYQKPG 62  
62 KSPQLLVYSAKTADGVPSRSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 121  
63 QSPKLLIYWASTRHGTGVPDRFTGSGSGTDFLTITSNVQSEDLADYFCQY-SSYRTFGG 121  
122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181  
122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181  
182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234  
182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234

## RESULT 10

US-10-275-180A-24  
; Sequence 24, Application US/10275180A  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APO  
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.002905  
; CURRENT APPLICATION NUMBER: US/10/275,180A  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
; OTHER INFORMATION: Synthetic Construct  
US-10-275-180A-24

Query Match 71.4%; Score 881.5; DB 6; Length 234;  
Best Local Similarity 73.4%; Pred. No. 2.7e-69;

Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

QY 2 SVLTQVALLLMTGARCIDIOMTQSPASLSASVGETVITTCRASGNIGNONYLAWYQQTQ 61  
Db 3 SLYVLVYTHYLFAGVGDIVMTQSHKFMSTSVGDRVSTICKASQDVGTAVAWYQQRPG 62

QY 62 KSPQLLVYSAKTLADGVPSRFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 121  
Db 63 QSPKLLIYMASTRHGTGVDRTFGSGGTDFTLTISNVQSEDLADYFCQY-SSYRTFGG 121

QY 122 TKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDNVKWKIDGSRONGVLN 181  
Db 122 TKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDNVKWKIDGSRONGVLN 181

QY 182 SWTQDQSDSTYSMSSTLTITKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
Db 182 SWTQDQSDSTYSMSSTLTITKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234

RESULT 11  
US-09-726-219A-188  
; Sequence 188, Application US/09726219A  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Medical Research Council  
; APPLICANT: McCafferty, John  
; APPLICANT: Pope, Anthony  
; APPLICANT: Johnson, Kevin  
; APPLICANT: Hoogenboom, Hendricus  
; APPLICANT: Griffiths, Andrew  
; APPLICANT: Jackson, Ronald  
; APPLICANT: Holliger, Kasper  
; APPLICANT: Marks, James  
; APPLICANT: Clackson, Timothy  
; APPLICANT: Chiswell, David  
; APPLICANT: Winter, Gregory  
; APPLICANT: Bonert, Timothy  
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
; FILE REFERENCE: 213839-00013  
; CURRENT APPLICATION NUMBER: US/09/726,219A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB 9015198.6  
; PRIOR FILING DATE: 1990-07-10  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9024503.6  
; PRIOR FILING DATE: 1990-11-12  
; PRIOR APPLICATION NUMBER: GB 9104744.9  
; PRIOR FILING DATE: 1991-03-06  
; PRIOR APPLICATION NUMBER: GB 9110549.4  
; PRIOR FILING DATE: 1991-05-15  
; PRIOR APPLICATION NUMBER: PCT/GB91/01134  
; PRIOR FILING DATE: 1991-07-10  
; PRIOR APPLICATION NUMBER: US 07/971,857  
; PRIOR FILING DATE: 1993-01-08  
; PRIOR APPLICATION NUMBER: US 08/484,893  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 272  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 188  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of Fab D1.3 from genetically engineered anti-hen egg-white lys  
; OTHER INFORMATION: ozyme (HEL) monoclonal antibody  
US-09-726-219A-188

Query Match 71.4%; Score 881; DB 5; Length 236;  
Best Local Similarity 73.8%; Pred. No. 3e-69;

Matches 169; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

QY 5 TOVLALLLMTGARCIDIOMTQSPASLSASVGETVITTCRASGNIGNONYLAWYQQTQ 64  
Db 7 TAAAGLLLLAAOPAMADIELTQSPASLSASVGETVITTCRASGNIGNONYLAWYQQTQ 66

QY 65 QLLVYSAKTLADGVPSRFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 124  
Db 67 QLLVYTTTTLADGVPSRFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 126

QY 125 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDNVKWKIDGSRONGVLN 184  
Db 127 EIKRTVAAPSVIFPPSDEQLKSGTASVCLNNFPKIDNVKWKIDGSRONGVLN 186

QY 185 DQDQSDSTYSMSSTLTITKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 233  
Db 187 EQDQSDSTYSMSSTLTITKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 235

RESULT 12  
US-10-236-051-4  
; Sequence 4, Application US/10236051  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: LETURCO, Didier J.  
; APPLICANT: MORIARTY, Ann M.  
; APPLICANT: ULEVITCH, Richard J.  
; APPLICANT: TOBIAS, Peter S.  
; APPLICANT: MATHISON, John C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT  
; FILE REFERENCE: SCRIP1140-4  
; CURRENT APPLICATION NUMBER: US/10/236,051  
; CURRENT FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: US 09/170,769  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: US 08/373,297  
; PRIOR FILING DATE: 1995-01-23  
; PRIOR APPLICATION NUMBER: PCT/US94/05898  
; PRIOR FILING DATE: 1994-05-27  
; PRIOR APPLICATION NUMBER: US 08/070,160  
; PRIOR FILING DATE: 1993-05-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Murine  
US-10-236-051-4

Query Match 68.5%; Score 845; DB 6; Length 215;  
Best Local Similarity 74.9%; Pred. No. 3.9e-66;  
Matches 161; Conservative 17; Mismatches 33; Indels 4; Gaps 1;

QY 24 MTQSPASLSASVGETVITTCRASGNIGNONYLAWYQQTQSGKSPQLLVYSAKTLADGV 79  
Db 1 MTQSPASLSAVLGLORAPYPCRASESDVSNSFLHWYQQRPGPKLLITRASNLQSG 60

QY 80 SRFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKLEIKRADAAPTYSIF 139  
Db 61 ARFGSGSRDFTLTINPVEADDAVATYCCQSNEDPTTSGGGTGGKLEIKRADAAPTYSIF 120

QY 140 PSSEQLTSGGASVVCFLNNFPKIDNVKWKIDGSRONGVLNWDQSDSTYSMSSTL 199  
Db 121 PSSEQLTSGGASVVCFLNNFPKIDNVKWKIDYSEKQVNSKWDQSDSTYSMSSTL 180

QY 200 TLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
Db 181 TLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 215

RESULT 13  
US-09-254-180C-132  
; Sequence 132, Application US/09254180C

```

GENERAL INFORMATION:
APPLICANT: OKUMURA, Ko
APPLICANT: EDA, Yasuyuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: USHIO, Yoshitaka
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
FILE REFERENCE: 050006-0055
CURRENT APPLICATION NUMBER: US/09/254,180C
CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/JP97/02983
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 271546/1996
PRIOR FILING DATE: 1996-09-20
PRIOR APPLICATION NUMBER: 231472/1996
PRIOR FILING DATE: 1996-09-02
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patent in version 3.1
SEQ ID NO 132
LENGTH: 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 216
TYPE: PRT
ORGANISM: Mouse
S-09-254-180C-132

Query Match 67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

y 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQOTQGKSPQLLYVSAKTLA 75
b 1 DVLMTQTLPLSLPVLGDAQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNR 60
y 76 DGVPSPRFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGTKLEIKRADAAPT 135
b 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYCYFCQGSHPFTFGSGTKLEIKRADAAPT 120
y 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 195
b 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTDDQSKDSTYS 180
y 196 SSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFN 231
b 181 SSTLTLTCKDEYERHNSYTCEATHKTSPIV
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Search completed: June 18, 2003, 16:48:37  
Job time : 28.6067 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2003, 16:44:27 ; Search time 144.935 seconds  
(without alignments)  
1040.930 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVQVALLLLWLTGARC.....EATHKTSPIVKSFNRNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA.Main.\*

1: /cgn2\_6/ptodata/1/paa/US06\_COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pcp.\*  
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11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pcp.\*  
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20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pcp.\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pcp.\*  
22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pcp.\*  
23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pcp.\*  
24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pcp.\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pcp.\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pcp.\*  
27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1234	100.0	234	21	US-09-770-916-4
2	1200	97.2	234	4	US-08-090-534-4
3	1165	94.4	228	21	US-09-791-537-58997
4	1146	92.9	228	21	US-09-791-537-58987
5	1127	91.3	234	21	US-09-791-537-127535
6	1116	90.4	214	21	US-09-791-537-104541

7	1099	89.1	214	21	US-09-791-537-44562	Sequence 44562, A
8	1092	88.5	214	21	US-09-791-537-13851	Sequence 13851, A
9	1075	87.1	214	21	US-09-791-537-13889	Sequence 13889, A
10	1057	85.7	214	21	US-09-791-537-97993	Sequence 97993, A
11	1029	83.4	213	21	US-09-791-537-105122	Sequence 105122, A
12	985	79.8	236	21	US-09-791-537-89134	Sequence 89134, A
13	974.5	79.0	235	21	US-09-791-537-114644	Sequence 114644, A
14	970	78.6	234	8	US-081480-120-4	Sequence 4, Appli
15	967	78.4	234	21	US-09-791-537-128696	Sequence 128696, A
16	966	78.3	234	21	US-09-791-537-55632	Sequence 55632, A
17	947	76.7	214	21	US-09-791-537-110636	Sequence 110636, A
18	940	76.2	214	21	US-09-791-537-87447	Sequence 87447, A
19	935	75.8	243	21	US-09-791-537-123349	Sequence 123349, A
20	933	75.6	214	21	US-09-791-537-88649	Sequence 88649, A
21	932	75.5	214	21	US-09-791-537-93651	Sequence 93651, A
22	931	75.4	214	21	US-09-791-537-29765	Sequence 29765, A
23	930	75.4	243	21	US-09-791-537-74441	Sequence 74441, A
24	925	75.0	214	21	US-09-791-537-52722	Sequence 52722, A
25	925	75.0	238	20	US-09-613-017-4	Sequence 4, Appli
26	925	75.0	238	23	US-09-903-327A-4	Sequence 4, Appli
27	920.5	74.6	213	21	US-09-791-537-27173	Sequence 27173, A
28	919.5	74.5	237	21	US-09-791-537-81230	Sequence 81230, A
29	918.5	74.4	237	21	US-09-791-537-51510	Sequence 51510, A
30	918	74.4	238	14	US-09-053-583-11	Sequence 11, Appl
31	918	74.4	238	18	US-09-408-646-11	Sequence 11, Appl
32	918	74.4	238	18	US-09-499-662-11	Sequence 11, Appl
33	918	74.4	238	26	US-10-216-484-11	Sequence 11, Appl
34	916	74.2	214	21	US-09-791-537-89445	Sequence 89445, A
35	915	74.1	220	21	US-09-791-537-14484	Sequence 14484, A
36	914	74.1	214	21	US-09-791-537-138888	Sequence 138888, A
37	914	74.1	216	10	US-08-665-839A-40	Sequence 40, Appl
38	914	74.1	216	10	US-08-665-839B-40	Sequence 40, Appl
39	910	73.7	212	21	US-09-791-537-107650	Sequence 107650, A
40	910	73.7	234	21	US-09-791-537-74535	Sequence 74535, A
41	909.5	73.7	235	3	US-07-904-074A-2	Sequence 2, Appli
42	909	73.7	214	21	US-09-791-537-66254	Sequence 66254, A
43	909	73.7	214	21	US-09-791-537-73158	Sequence 73158, A
44	909	73.7	214	21	US-09-791-537-85310	Sequence 85310, A
45	909	73.7	218	21	US-09-791-537-32984	Sequence 32984, A

#### ALIGNMENTS

RESULT 1  
US-09-770-916-4  
; Sequence 4, Application US/09770916  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Dara W.  
; APPLICANT: Wiener-Kronish, Jeannine  
; APPLICANT: Yahr, Timothy L.  
; APPLICANT: Sawa, Teiji  
; APPLICANT: Fritz, Robert B.  
; TITLE OF INVENTION: Method of and compositions for immunization with the  
; FILE REFERENCE: 650053.91487  
; CURRENT APPLICATION NUMBER: US/09/770,916  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/448,339  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/109,952  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 60/126,794  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-770-916-4  
Query Match 100.0%; Score 1234; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 5.7e-100;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLLTGARGDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
|||||  
1 MSVLTQVLAALLLLLTGARGDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
|||||  
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYTCQHFWSPTPTFGG 120  
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121 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 180  
|||||  
121 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 180  
|||||  
181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
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181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
|||||

## RESULT 2

US-08-090-534-4  
; Sequence 4, Application US/08090534  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurle, Mark  
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
; TITLE OF INVENTION: Disorders in Man  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; ADDRESSEE: Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLYING DATE: 19930719  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: SEC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-270-5015  
TELEFAX: 215-270-5090  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-090-534-4

Query Match 97.2%; Score 1200; DB 4; Length 234;  
Best Local Similarity 97.0%; Pred. No. 5.7e-97;  
Matches 227; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLLTGARGDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
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1 MSVLTQVLAALLLLLTGARGDIQMTQSPASLSASVGETVITTCRASGNIHNYLWYQKQ 60  
|||||

Qy 61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYTCQHFWSPTPTFGG 120  
Db |||||  
Qy 61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYTCQHFWSPTPTFGG 120  
Db |||||  
Qy 121 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 180  
Db |||||  
Qy 121 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 180  
Db |||||  
Qy 181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
Db |||||  
Qy 181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
Db |||||

## RESULT 3

US-09-791-537-58997  
; Sequence 58997, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 58997  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-58997

Query Match 94.4%; Score 1165; DB 21; Length 228;  
Best Local Similarity 95.6%; Pred. No. 6.6e-94;  
Matches 218; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 7 VLALLLLWLTGARGDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQKSPQL 66  
Db |||||  
Qy 1 VLGLLLWLTGARGDIQMTQSPASLSASVGETVITTCRASGNIHNYLAWYQQTQKSPQL 60  
Db |||||  
Qy 67 LVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYTCQHFWSPTPTFGGSKLEI 126  
Db |||||  
Qy 61 LVYNAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGTYYCHHFWPTPTFGGSKLEI 120  
Db |||||  
Qy 127 KRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQ 186  
Db |||||  
Qy 121 KRADAAPTIVSILPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQ 180  
Db |||||  
Qy 187 DSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 234  
Db |||||  
Qy 181 DSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 228  
Db |||||

## RESULT 4

US-09-791-537-58987  
; Sequence 58987, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 58987  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-58987

Query Match 92.9%; Score 1146; DB 21; Length 228;  
Best Local Similarity 94.3%; Pred. No. 3.1e-92;  
Matches 215; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 7 VLALLLWLTGARDIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTGKSPQL 66  
DB 1 VLGLLLWLTGARDIQMTQSPASLSAFVGETVTITCRASGNIHNYLAWYQQTGKSPRV 60

QY 67 LVYSAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTHKLEI 126  
DB 61 LVYAKTLVDGVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSIPTPTFGGTHKLEI 120

QY 127 KRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVLSNWDQ 186  
DB 121 KRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVLSNWDQ 180

QY 187 DSKDSTYSMSSTLTATKDEYERHNSYTCETHKTSPIVKSFNREC 234  
DB 181 DSKDSTYSMSSTLTATKDEYERHNSYTCETHKTSPIVKSFNREC 228

RESULT 5  
US-09-791-537-127535  
; Sequence 127535, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 127535  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-127535

Query Match 91.3%; Score 1127; DB 21; Length 234;  
Best Local Similarity 91.9%; Pred. No. 1.5e-90;  
Matches 215; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSVLQVALLLWLTGARDIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTQ 60  
DB 1 MSVPTQVLLGLLLWLTGARDIQMTQSPASLSVSGESVTITCRASENIYSLNLTQYQKQ 60

QY 61 GKSPOLLVYSAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 120  
DB 61 GKSPOLLVYATKLVDPVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWDTPPTFGG 120

QY 121 GPKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVYL 180  
DB 121 GPKLEMKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVYL 180

QY 181 NSWTDQSKDSTYSMSSTLTATKDEYERHNSYTCETHKTSPIVKSFNREC 234  
DB 181 NSWTDQSKDSTYSMSSTLTATKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 6  
US-09-791-537-104541  
; Sequence 104541, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 104541  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: pdb 1WEJL  
US-09-791-537-104541

Query Match 90.4%; Score 1116; DB 21; Length 214;  
Best Local Similarity 98.1%; Pred. No. 1.3e-89;  
Matches 210; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTGKSPQLLYSAKTLADGVPS 80  
DB 1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQTGKSPQLLYVNAKTLADGVPS 60

QY 81 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTHKLEIKRADAAPTYSIFPP 140  
DB 61 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTHKLEIKRADAAPTYSIFPP 120

QY 141 SSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVLSNWDQSKDSTYSMSSTLT 200  
DB 121 SSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVLSNWDQSKDSTYSMSSTLT 180

QY 201 LTKDEYERHNSYTCETHKTSPIVKSFNREC 234  
DB 181 LTKDEYERHNSYTCETHKTSPIVKSFNREC 214

RESULT 7  
US-09-791-537-44562  
; Sequence 44562, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 44562  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: pdb 1FDLL  
US-09-791-537-44562

Query Match 89.1%; Score 1099; DB 21; Length 214;  
Best Local Similarity 97.2%; Pred. No. 3.9e-88;  
Matches 208; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTGKSPQLLYSAKTLADGVPS 80  
DB 1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQTGKSPQLLYVYTTTLADGVPS 60

QY 81 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTHKLEIKRADAAPTYSIFPP 140  
DB 61 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGTHKLEIKRADAAPTYSIFPP 120

QY 141 SSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVLSNWDQSKDSTYSMSSTLT 200  
DB 121 SSEQLTSGGASVVCFLNNFPKIDINVKKIDGSEONGVLSNWDQSKDSTYSMSSTLT 180

QY 201 LTKDEYERHNSYTCETHKTSPIVKSFNREC 234  
DB 181 LTKDEYERHNSYTCETHKTSPIVKSFNREC 214

RESULT 8

S-09-791-537-13851  
Sequence 13851, Application US/09791537  
GENERAL INFORMATION:  
APPLICANT: Bionomix, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER  
FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791.537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13851  
LENGTH: 214  
TYPE: PRT  
ORGANISM: pdb 1C1CC  
S-09-791-537-13851

Query Match 88.5%; Score 1092; DB 21; Length 214;  
Best Local Similarity 96.3%; Pred. No. 1.6e-87;  
Matches 206; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
21 DIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQCKSPQLLYVSAKTLADGVPS 80  
|||||  
1 DIQMTQSPASLSASVGETVITTCRASGNIHNYLAWYQKQKSPQLLYVTTTLADGVPS 60  
|||||  
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGKTKLEIKRADAAPTVSIFPP 140  
|||||  
61 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGKTKLEIKRADAAPTVSIFPP 120  
|||||  
141 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 200  
|||||  
121 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 180  
|||||  
201 LTKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234  
|||||  
181 LTKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 214  
|||||

RESULT 9  
S-09-791-537-138889  
Sequence 13889, Application US/09791537  
GENERAL INFORMATION:  
APPLICANT: Bionomix, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER  
FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791.537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13889  
LENGTH: 214  
TYPE: PRT  
ORGANISM: pdb 1KB5L  
S-09-791-537-138889

Query Match 87.1%; Score 1075; DB 21; Length 214;  
Best Local Similarity 94.9%; Pred. No. 5.1e-86;  
Matches 203; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
21 DIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQCKSPQLLYVSAKTLADGVPS 80  
|||||  
1 DIQMTQSPASLSASVGETVITTCRASGNIYSLAWYQKQKSPQLLYVNAKTLGEGVPS 60  
|||||  
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGKTKLEIKRADAAPTVSIFPP 140  
|||||  
61 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGKTKLEIKRADAAPTVSIFPP 120  
|||||  
141 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 200  
|||||

Db 121 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 180  
|||  
Qy 201 LTKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234  
|||||  
Db 181 LTKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 214  
|||||

## RESULT 10

US-09-791-537-97993  
Sequence 97993, Application US/09791537  
GENERAL INFORMATION:  
APPLICANT: Bionomix, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER  
FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791.537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 97993  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Mus sp  
US-09-791-537-97993

Query Match 85.7%; Score 1057; DB 21; Length 214;  
Best Local Similarity 93.0%; Pred. No. 2e-84; 7; Indels 0; Gaps 0;  
Matches 199; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
21 DIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQCKSPQLLYVSAKTLADGVPS 80  
|||  
1 ELQMTQSPASLSASVGETVITTCRASGNIYSLAWYQKQKSPQLLYVNAKTLAEGVPS 60  
|||  
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGKTKLEIKRADAAPTVSIFPP 140  
|||  
61 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGKTKLEIKRADAAPTVSIFPP 120  
|||  
141 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 200  
|||  
121 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 180  
|||  
Qy 201 LTKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234  
|||  
Db 181 LTKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 214  
|||

## RESULT 11

US-09-791-537-105122  
Sequence 105122, Application US/09791537  
GENERAL INFORMATION:  
APPLICANT: Bionomix, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER  
FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791.537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 105122  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-791-537-105122

Query Match 83.4%; Score 1029; DB 21; Length 213;  
Best Local Similarity 90.6%; Pred. No. 5.7e-82;  
Matches 193; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 21 DIQMTSPASLSASVGETVITCRASGNIGNIYLAQYQOTQKSPQLLVYSAKTLADGVP 80  
 Db 1 DIQMTSPASLSASVGETVITCRASGNIGNIYLAQYQOTQKSPQLLVYNAKDLAEGVPS 60  
 QY 81 RFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTFGGKLEIKRADAAPTVSIFPP 140  
 Db 61 RFGSGAGTQSLRINSLOPEDFGSYCYQHFWSTPTFGGKLEIKRADAAPTVSIFPP 120  
 QY 141 SSELTSGGASVVCFLNNYPRKDVNKKIDGSRQNGVLSNWTDDSKDSTYSMSSTLT 200  
 Db 121 SSELTSGGASVVCFLNNYPRKDVNKKIDGSRQNGVLSNWTDDSKDSTYSMSSTLT 180  
 QY 201 LTKDEYERHNSYTCETHKTSSTSPIVKSFNRNE 233  
 Db 181 LTRDEYERHNSYTCETHKTSSTSPIVKSFNRNE 213

RESULT 12  
 US-09-791-537-89134  
 ; Sequence 89134, Application US/09791537  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bionomix, Inc.  
 ; APPLICANT: Debe, Derek  
 ; APPLICANT: Danzer, Joseph  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
 ; TITLE OF INVENTION: METHODS OF USE THEREOF  
 ; FILE REFERENCE: 261/210  
 ; CURRENT APPLICATION NUMBER: US/09/791,537  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 89134  
 ; LENGTH: 236  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-791-537-89134

Query Match 79.8%; Score 985; DB 21; Length 236;  
 Best Local Similarity 79.5%; Pred. No. 4.9e-78;  
 Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSVLTVQVALLLMTGARDIOMTQSPASLSASVGETVITCRASGNIGNIYLAQYQOTQ 60  
 Db 3 MTRPAQFLGILLWFGMKDKIMTQSPSMVSLGERVITTCASQDINSYLSWFQK 62  
 QY 61 GKSPQLLVYSAKTLADGVPFRSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTFGG 120  
 Db 63 GKSPKTLIYRANRLVDGVPFRSGSGGQDYSLTISSEYEDMGIIYCYQYDFPPTFG 122  
 QY 121 GKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNYPRKDVNKKIDGSRONGVL 180  
 Db 123 GKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNYPRKDVNKKIDGSRONGVL 182  
 QY 181 NSWTDQSDKSTYSMSSTLTATKDEYERHNSYTCETHKTSSTSPIVKSFNRNEC 234  
 Db 183 NSWTDQSDKSTYSMSSTLTATKDEYERHNSYTCETHKTSSTSPIVKSFNRNEC 236

RESULT 13  
 US-09-791-537-114644  
 ; Sequence 114644, Application US/09791537  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bionomix, Inc.  
 ; APPLICANT: Debe, Derek  
 ; APPLICANT: Danzer, Joseph  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
 ; TITLE OF INVENTION: METHODS OF USE THEREOF  
 ; FILE REFERENCE: 261/210  
 ; CURRENT APPLICATION NUMBER: US/09/791,537  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 114644

; LENGTH: 235  
 ; TYPE: PRT  
 ; ORGANISM: synthetic construct  
 US-09-791-537-114644

Query Match 79.0%; Score 974.5; DB 21; Length 235;  
 Best Local Similarity 80.9%; Pred. No. 4.1e-77;  
 Matches 190; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 1 MSVLTVQVALLLMTGARDIOMTQSPASLSASVGETVITCRASGNIGNIYLAQYQOT 59  
 Db 1 MKQSTIALALLPLFTVTRKADIELTQSPALMAASVGETVITTCGASENIYALNWTQ 60  
 QY 60 QKSPQLLVYSAKTLADGVPFRSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTFG 119  
 Db 61 QKSPQLLVYSAKTLADGVPFRSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTFG 120  
 QY 120 GGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNYPRKDVNKKIDGSRONGV 179  
 Db 121 AGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNYPRKDVNKKIDGSRONGV 180  
 QY 180 LNSWTDQSDKSTYSMSSTLTATKDEYERHNSYTCETHKTSSTSPIVKSFNRNEC 234  
 Db 181 LNSWTDQSDKSTYSMSSTLTATKDEYERHNSYTCETHKTSSTSPIVKSFNRNEC 235

RESULT 14  
 US-08-480-120-4  
 ; Sequence 4, Application US/08480120  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Joliffe, Linda K.  
 ; APPLICANT: Zivin, Robert A.  
 ; APPLICANT: Pulito, Virginia L.  
 ; TITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR  
 ; TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/480,120  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,346  
 ; REFERENCE/DOCKET NUMBER: 9598  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 234 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-480-120-4

Query Match 78.6%; Score 970; DB 8; Length 234;  
 Best Local Similarity 78.3%; Pred. No. 1e-76;  
 Matches 183; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSVLTVQVALLLMTGARDIOMTQSPASLSASVGETVITCRASGNIGNIYLAQYQOT 60

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1 MRAPAQFFGILLWFGIRCDIKMTQSPSSWYASLGERVTITCKASQDIRKYLNWYQOKP 60
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTOYSLKINSLOPEDFGSYCOHFWSTPYTFGG 120
61 WKSPKTLIYVATSLADGVPSRFGSGSGQDYSLTISLESDDTATYYCLOHGESPYPYTFGG 120
121 GTKLEIKRADAAPTSTIFFPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 180
121 GTKLEINRADAAPTSTIFFPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 180
181 NSWTQDQSKDSTYSMSSTLTLTDEYERHNSYCEATHKTSTPIVKSFNKNEC 234
181 NSWTQDQSKDSTYSMSSTLTLTDEYERHNSYCEATHKTSTPIVKSFNKNEC 234

RESULT 15
US-09-791-537-128696
Sequence 128696, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patent in version 3.0
SEQ ID NO 128696
LENGTH: 234
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-128696
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Query Match 78.4%; Score 967; DB 21; Length 234;
Best Local Similarity 77.8%; Pred. No. 1.9e-76;
Matches 182; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

1 MSVLTQVLAALLLWLTGARDIQMTQSPASLSASVGETVTITCRASGNIONYLAWTQQTQ 60
1 MRTPAQFLGILLWFGIRCDIKMTQSPSSWYASLGERVTISCKASQDINSYLTWFQOKP 60
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTOYSLKINSLOPEDFGSYCOHFWSTPYTFGG 120
61 GKSPKTLIYVATSLADGVPSRFGSGSGQDYSLTISLESDDTATYYCLOHGESPYPYTFGG 120
121 GTKLEIKRADAAPTSTIFFPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 180
121 GTKLEINRADAAPTSTIFFPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 180
181 NSWTQDQSKDSTYSMSSTLTLTDEYERHNSYCEATHKTSTPIVKSFNKNEC 234
181 NSWTQDQSKDSTYSMSSTLTLTDEYERHNSYCEATHKTSTPIVKSFNKNEC 234
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Search completed: June 18, 2003, 16:56:49  
Job time : 146.935 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: June 18, 2003, 16:46:17 ; Search time 22.0197 seconds  
(without alignments)  
1149.899 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVALLLLWLITGARC.....EATHKTSPIVKSFNREC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_5/ptodata/2/pubaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	925	75.0	238	9	US-09-903-327A-4
2	918	74.4	238	9	US-10-216-484-11
3	883.5	71.6	235	9	US-09-795-515-5
4	870	70.5	672	9	US-09-900-766-1
5	816	66.1	236	9	US-10-006-593-69
6	808	65.5	234	10	US-09-740-002-24
7	806	65.3	237	9	US-10-194-975-109
8	799	64.7	236	10	US-09-859-053-30
9	772.5	62.6	234	10	US-09-740-002-26
10	771	62.5	234	10	US-09-800-729-150
11	766	62.1	214	9	US-10-153-382-19
12	761	61.7	245	9	US-09-797-941A-6
13	756.5	61.3	235	10	US-09-800-729-152
14	754	61.1	237	9	US-10-020-786-8
15	754	61.1	237	9	US-10-227-694-4
16	751	60.9	237	9	US-10-227-694-1
17	751	60.9	237	10	US-09-056-160B-100
18	751	60.9	237	10	US-09-940-166A-5
19	751	60.9	491	12	US-10-011-125-2

## ALIGNMENTS

### RESULT 1

US-09-903-327A-4  
; Sequence 4, Application US/09903327A  
; Patent No. US20020164333A1  
; GENERAL INFORMATION:  
; APPLICANT: Nemerow, Glen R.  
; APPLICANT: Li, Erquang  
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR  
; TITLE OF INVENTION: GENE  
; TITLE OF INVENTION: DELIVERY  
; FILE REFERENCE: 22908-1228  
; CURRENT APPLICATION NUMBER: US/09/903,327A  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 09/613,017  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody  
US-09-903-327A-4

20	744	60.3	214	10	US-09-940-166A-2	Sequence 2, Appli
21	744	60.3	214	10	US-09-811-384-11	Sequence 11, Appl
22	744	60.3	237	9	US-10-020-786-10	Sequence 10, Appl
23	744	60.3	240	10	US-09-799-514-8	Sequence 8, Appli
24	743	60.2	238	9	US-10-216-484-127	Sequence 127, App
25	742	60.1	238	9	US-10-216-484-131	Sequence 131, App
26	739	59.9	238	9	US-10-216-484-129	Sequence 129, App
27	736	59.6	214	9	US-10-253-366-1	Sequence 1, Appli
28	732	59.3	218	10	US-09-920-171-15	Sequence 15, Appl
29	732	59.3	218	10	US-09-920-171-17	Sequence 17, Appl
30	732	59.3	218	10	US-09-920-171-19	Sequence 19, Appl
31	732	59.3	218	10	US-09-920-171-24	Sequence 24, Appl
32	732	59.3	239	10	US-09-825-012-9	Sequence 9, Appli
33	730	59.2	218	9	US-09-1925-179-9	Sequence 9, Appli
34	730	59.2	218	10	US-09-802-077-9	Sequence 9, Appli
35	730	59.2	218	10	US-09-802-096-9	Sequence 9, Appli
36	730	59.2	218	10	US-09-920-171-13	Sequence 13, Appl
37	729.5	59.1	235	10	US-09-910-059-52	Sequence 52, Appl
38	727	58.9	212	12	US-10-011-125-5	Sequence 211, App
39	725.5	58.8	213	9	US-09-1996-288-211	Sequence 2, Appli
40	725.5	58.8	213	9	US-09-1996-265-211	Sequence 5, Appli
41	724	58.7	218	10	US-09-917-410-2	Sequence 211, App
42	724	58.7	220	10	US-09-917-410-5	Sequence 2, Appli
43	723.5	58.6	235	10	US-09-910-059-99	Sequence 5, Appli
44	723	58.6	214	9	US-09-1875-221A-128	Sequence 99, Appl
45	723	58.6	214	10	US-09-949-559-128	Sequence 128, App

Query Match 75.0%; Score 925; DB 9; Length 238;  
Best Local Similarity 73.1%; Pred. No. 5.9e-39;  
Matches 174; Conservative 27; Mismatches 33; Indels 4; Gaps 1;  
QY 1 MSVLTVALLLLWLITGARDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWY 56  
Db 1 MEPTDILLWLLVWPGSTGDIVLTQSPASLSVSLGQRATISKASVSVDYDGSYNNWY 60  
QY 57 QQTGKSPQLLVYSAKTLADVPVSRFSGSGSGTQYSLKINSLOPFDGYSYQCQHFWSPTY 116  
Db 61 QKPGQPKLLIIVAASNLGSIIPARFSGSGSGTDTFLNIHPVEEDATYTCQQTNEPDW 120  
QY 117 TFGGGTKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGDSERQ 176  
Db 121 TFGGGTKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGDSERQ 180

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177 NGVLSWTDQSDKSDSYMSSTLTLTQKDEYERHNSYTCETHKTSPIVKSFNREC 234
181 NGVLSWTDQSDKSDSYMSSTLTLTQKDEYERHNSYTCETHKTSPIVKSFNREC 238

RESULT 2
Sequence 11, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
LENGTH: 238
TYPE: PRT
ORGANISM: Mus musculus
US-10-216-484-11

Query Match 74.4%; Score 918; DB 9; Length 238;
Best Local Similarity 72.3%; Pred. No. 1.3e-38;
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

1 MSVLTQVLALLLWLTG--ARCDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWY 56
1 METDTILLWMLWIPGSTGDIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNY 60

57 QQTGKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPT 116
61 QQKPGQPPLLIYAASNLSEGPAPFSGSGTDTLTNIHPVEEDAATYYCQGSNEDPR 120

117 TFGGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQ 176
121 TFGGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQ 180

177 NGVLSWTDQSDKSDSYMSSTLTLTQKDEYERHNSYTCETHKTSPIVKSFNREC 234
181 NGVLSWTDQSDKSDSYMSSTLTLTQKDEYERHNSYTCETHKTSPIVKSFNREC 238

RESULT 3
US-09-795-515-5
Sequence 5, Application US/09795515
Publication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

us-09-795-515-5
Sequence 1, Application US/09900766
Publication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 672
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(672)
OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 70.5%; Score 870; DB 9; Length 672;
Best Local Similarity 73.8%; Pred. No. 6.5e-36;
Matches 169; Conservative 20; Mismatches 36; Indels 4; Gaps 1;
```



QY 5 TQVALLLLWLTGARCIDIQMTQSPASLSASVGETVTITCRASGNIONYLANWYQQTGKSP 64  
Db 447 TSLISLYLT---SVMTQTPTSLVSGADRVITITCKASQSVNDVAVYQKPGQSP 502  
QY 65 QLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGTKL 124  
Db 503 KLLSYSSRVAGVPDRFSGSGYGTDFTLTSSVQAEAAVYFCQDYNSTPTFTGGTKL 562  
QY 125 EIKRADAAPTIVSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRONGVLSNWT 184  
Db 563 EIKRADAAPTIVSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRONGVLSNWT 622  
QY 185 DQDSKDSYSTSMSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNNE 233  
Db 623 DQDSKDSYSTSMSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNNE 671

## RESULT 5

US-10-006-593-69  
; Sequence 69, Application US/10006593  
; Publication No. US20030049683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowditch, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
; FILE REFERENCE: 1087-2  
; CURRENT APPLICATION NUMBER: US/10/006,593  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/251,448  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/288,889  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,068  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized antibody light chain  
US-10-006-593-69

Query Match 66.1%; Score 816; DB 9; Length 236;  
Best Local Similarity 66.2%; Pred. No. 1.3e-33;  
Matches 155; Conservative 28; Mismatches 51; Indels 0; Gaps 0;  
QY 1 MSVLTQVALLLLWLTGARCIDIQMTQSPASLSASVGETVTITCRASGNIONYLANWYQQTQ 60  
Db 3 MRVPAQLLGLLLWLRGARCIDIQMTQSPSSLSASVGDRTVITCGASENIYCALNWKYQKP 62  
QY 61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGG 120  
Db 63 GKAPKLLIYGATNLADGVPSRFGSGSGTDFTLTSSLOPEDFATYICQVNLNPTFTFGQ 122  
QY 121 GTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVKWIDGSRONGVL 180  
Db 123 GTKVEIKRTVAAPSVFIPFSPDQLSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQ 182  
QY 181 NSWTDQDSKDSYSTSMSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNNEC 234  
Db 183 ESVTEQDSKDSYSTSLSTLTSLRADYKHKYACEVTHQGLSSPVTKSFNRGEC 236

## RESULT 6

US-09-740-002-24  
; Sequence 24, Application US/09740002  
; Patent No. US20020001798A1  
; GENERAL INFORMATION:  
; APPLICANT: BRAMS, PETER  
; APPLICANT: MORROW, PHILLIP

; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-02/5759  
; CURRENT APPLICATION NUMBER: US/09/740,002  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/335,697  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 08/488,376  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-740-002-24

Query Match 65.5%; Score 808; DB 10; Length 234;  
Best Local Similarity 64.5%; Pred. No. 3.1e-33;  
Matches 151; Conservative 29; Mismatches 54; Indels 0; Gaps 0;  
QY 1 MSVLTQVALLLLWLTGARCIDIQMTQSPASLSASVGETVTITCRASGNIONYLANWYQQTQ 60  
Db 1 METPAQLLGLLLWLRGARCIDIQMTQSPSSLSASVGDRTVITCRAGQRIASLYLNWYQHP 60  
QY 61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGG 120  
Db 61 GKAPKLLIYGATNLADGVPSRFGSGSGTDFTLTSSLOPEDFATYICQVNLNPTFTFGP 120  
QY 121 GTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVKWIDGSRONGVL 180  
Db 121 GTKVEIKRTVAAPSVFIPFSPDQLSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQ 180  
QY 181 NSWTDQDSKDSYSTSMSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNNEC 234  
Db 181 ESVTEQDSKDSYSTSLSTLTSLRADYKHKYACEVTHQGLSSPVTKSFNRGEC 234

## RESULT 7

US-10-194-975-109  
; Sequence 109, Application US/10194975  
; Publication No. US20030039649A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: Super Humanized Antibodies  
; FILE REFERENCE: 501231.01  
; CURRENT APPLICATION NUMBER: US/10/194,975  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 109  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized chimeric D1.3 antibody  
US-10-194-975-109

Query Match 65.3%; Score 806; DB 9; Length 237;  
Best Local Similarity 68.5%; Pred. No. 4e-33;  
Matches 150; Conservative 24; Mismatches 45; Indels 0; Gaps 0;  
QY 16 TGARCIDIQMTQSPASLSASVGETVTITCRASGNIONYLANWYQQTGKSPQLLVYSAKTLA 75  
Db 19 TNAYAAIRMTQSPSSLSASVGDRTVITCRASGNINHLYLANWYQKAPKLFYITTTLA 78  
QY 76 DGVPSSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGTKLEIKRADAAPTIV 135  
Db 79 DGVPSSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGTKLEIKRADAAPTIV 138

136 SIFPPSEQLTSGASVVCFLNFPKIDINVKWIDGSRQNGVLNSWTDQDSKDSYSTSM 195  
139 FIFPPDEQLKSTASVYCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 198  
196 SSTLTLTCKDEYERHNSYTCETHKTSPTSPVKSFNRECEC 234  
199 SSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 8  
Sequence 30, Application US/09859053  
Patent No. US20020102658A1  
GENERAL INFORMATION:  
APPLICANT: Tsuji, Takashi  
APPLICANT: Tezuka, Katsunari  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
FILE REFERENCE: 06501-079001  
CURRENT APPLICATION NUMBER: US/09/859,053  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: JP 2001-99508  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: JP 2000-147116  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-859-053-30

Query Match 64.78; Score 799; DB 10; Length 236;  
Best Local Similarity 64.58; Pred. No. 8.7e-33;  
Matches 151; Conservative 30; Mismatches 53; Indels 0; Gaps 0;  
1 MSVLTQVLALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
3 MRVPAQLLGLLLWLFPGSRCDIQMTQSPSSVSVSGVDRVITTCRASGISRLAWYQOKP 62  
61 GKSPQLLYVSAKTLADGVPSRFGSGGTQYSLKINSIQPEDFGSYCQHFWSPTFTFG 120  
63 GKAPKLLIYVASSLSQSGVPSRFGSGGTDTFTLTISLQPEDFATYTCQANSFPWTFGQ 122  
121 GTKLEIKRADAAPTVSIFPPSSEQLTSGASVVCFLNFPKIDINVKWIDGSRQNGVL 180  
123 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNFPYPREAKVQWKVDNALQSGNSQ 182  
181 NSWTDQDSKSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPTSPVKSFNRECEC 234  
183 ESVTEQDSKSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 9  
Sequence 26, Application US/09740002  
Patent No. US20020001798A1  
GENERAL INFORMATION:  
APPLICANT: BRAMS, PETER  
APPLICANT: MORROW, PHILLIP  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF  
FILE REFERENCE: 037003-0275759  
CURRENT APPLICATION NUMBER: US/09/740,002  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/335,697  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 08/488,376  
PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 234  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-740-002-26

Query Match 62.6%; Score 772.5; DB 10; Length 234;  
Best Local Similarity 62.7%; Pred. No. 1.7e-31;  
Matches 146; Conservative 37; Mismatches 49; Indels 1; Gaps 1;  
1 MSVLTQVLALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
3 MRVPAQLLGLLLWLTGARDIQMTQSPSSLSASVSGVDRVITTCRASGISRLAWYQOKP 62  
61 GKSPQLLYVSAKTLADGVPSRFGSGGTQYSLKINSIQPEDFGSYCQHFWSPTFTFG 120  
63 GKAPKLLIYVASSLSQSGVPSRFGSGGTDTFTLTISLQPEDFATYTCQANSFPWTFGQ 122  
121 GTKLEIKRADAAPTVSIFPPSSEQLTSGASVVCFLNFPKIDINVKWIDGSRQNGVL 180  
122 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNFPYPREAKVQWKVDNALQSGNSQ 181  
181 NSWTDQDSKSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPTSPVKSFNRECEC 233  
182 ESVTEQDSKSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 10  
US-09-800-729-150  
Sequence 150, Application US/09800729  
Patent No. US20020068319A1  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: 32 Human secreted proteins  
FILE REFERENCE: P2044P1  
CURRENT APPLICATION NUMBER: US/09/800,729  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: PCT/US00/26013  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/155,709  
PRIOR FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 150  
LENGTH: 234  
TYPE: PRT  
ORGANISM: Homo sapiens  
NAME/KEY: SITE  
LOCATION: (120)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-800-729-150

Query Match 62.5%; Score 771; DB 10; Length 234;  
Best Local Similarity 61.1%; Pred. No. 2e-31;  
Matches 143; Conservative 36; Mismatches 55; Indels 0; Gaps 0;  
1 MSVLTQVLALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
1 MRVPAQLLGLLLWLTGARDIQMTQSPSSLSASVSGVDRVITTCRASGISRLAWYQOKP 60  
61 GKSPQLLYVSAKTLADGVPSRFGSGGTQYSLKINSIQPEDFGSYCQHFWSPTFTFG 120  
63 GKAPKLLIYVASSLSQSGVPSRFGSGGTDTFTLTISLQPEDFATYTCQANSFPWTFGQ 122  
121 GTKLEIKRADAAPTVSIFPPSSEQLTSGASVVCFLNFPKIDINVKWIDGSRQNGVL 180  
122 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNFPYPREAKVQWKVDNALQSGNSQ 180  
181 NSWTDQDSKSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPTSPVKSFNRECEC 234

Db 181 ESVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 11

US-10-153-382-19

Sequence 19, Application US/10153382

Publication No. US20030086930A1

GENERAL INFORMATION:

APPLICANT: PFIZER PRODUCTS INC.

TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES

FILE REFERENCE: PC23019A

CURRENT APPLICATION NUMBER: US/10/153,382

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: 60/293042

PRIOR FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 214

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-382-19

Query Match 62.1%; Score 766; DB 9; Length 214;

Best Local Similarity 65.9%; Pred. No. 3.4e-31;

Matches 141; Conservative 32; Mismatches 41; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITTCRASGNITQNYLAWYQQTQKSPQLLYSAKTLADGVPS 80

Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQINSYLDWYQKPKAPKLLIYAASLSQGVPS 60

QY 81 RPSGSGGTQVSLKINSLOPEDFGSYCOHFWSTPTTGGGKLEIKRADAAPTYSIIPP 140

Db 61 RPSGSGGTQVSLKINSLOPEDFGSYCOHFWSTPTTGGGKLEIKRADAAPTYSIIPP 120

QY 141 SSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRONGVLSNWTQDSDKSTYSMSSTLT 200

Db 121 SDEQLKSTASVVCFLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSLSSTLT 180

QY 201 LTKDEYRHNSYTCETHKTSPTIVKSFNRNEC 234

Db 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 12

US-09-797-941A-6

Sequence 6, Application US/09797941A

Patent No. US20020164788A1

GENERAL INFORMATION:

APPLICANT: ELLIS, JONATHAN H.

LEWIS, ALAN P.

TITLE OF INVENTION: HUMANISED ANTIBODIES TO CD38

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/797,941A

FILING DATE: 05-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/849,410

FILING DATE: 30-MAY-1997

APPLICATION NUMBER: PCT/GB95/02777

FILING DATE: 28-NOV-1995

APPLICATION NUMBER: GB 9424449.8

FILING DATE: 02-DEC-1994

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-797-941A-6

Query Match 61.7%; Score 761; DB 9; Length 245;

Best Local Similarity 61.8%; Pred. No. 6.6e-31;

Matches 141; Conservative 32; Mismatches 55; Indels 0; Gaps 0;

QY 7 VIALLLLMTGARCIDIQMTQSPASLSASVGETVITTCRASGNITQNYLAWYQQTQKSPQL 66

Db 18 IILFLVATATGVHSDIQMTQSPSSLSASVGDRTVITCKASEDIYNRLTWQKPKRAPKL 77

QY 67 LYSAKTLADGVPSRPSGSGGTQVSLKINSLOPEDFGSYCOHFWSTPTTGGGKLEI 126

Db 78 LLSGATSLTGVPSRPSGSGGTQVSLKINSLOPEDFGSYCOHFWSTPTTGGGKLEI 137

QY 127 KRADAAPTYSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRONGVLSNWTQ 186

Db 138 KRTVAAPSVFIIPPSDEQLKSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQESVTEQ 197

QY 187 DSKDSTYSMSSTLTLTCKDEVERHNSYTCETHKTSPTIVKSFNRNEC 234

Db 198 DSKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 245

RESULT 13

US-09-800-729-152

Sequence 152, Application US/09800729

Patent No. US20020068319A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 32 Human secreted proteins

FILE REFERENCE: P2044P1

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: PCT/US00/26013

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 152

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-09-800-729-152

Query Match 61.3%; Score 756.5; DB 10; Length 235;

Best Local Similarity 62.0%; Pred. No. 1.1e-30;

Matches 145; Conservative 31; Mismatches 57; Indels 1; Gaps 1;

QY 1 MSVLTVLALLLLMTGARCIDIQMTQSPASLSASVGETVITTCRASGNITQNYLAWYQQTQ 60

Db 3 MRVPAQLGLGLLLWLRGARCQMOTQSPSSLSASVGDRTVITTCRTSQSIGKFLNNYQKPK 62

QY 61 GKSPOLLVYSAKTLADGVPSRPSGSGGTQVSLKINSLOPEDFGSYCOHFWSTPTTGGG 120

Db 63 GQAPKLLISGASILQTVPSRPSGSGSATYFTLTINDHPEDSATYTCQDITTP-LFGQ 121

QY 121 GTKLEIKRADAAPTYSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRONGVL 180

Db 122 GTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQ 181

QY 181 NSWTQDSDKSTYSMSSTLTLTCKDEYRHNSYTCETHKTSPTIVKSFNRNEC 234

db 182 ESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 14

JS-10-020-786-8

Sequence 8, Application US/10020786

Publication No. US20030073164A1

GENERAL INFORMATION:

APPLICANT: Simmons, Laura C.

APPLICANT: Klimowski, Laura

APPLICANT: Reilly, Dorothea

APPLICANT: Yansura, Daniel G.

TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF

FILE REFERENCE: P1793R1

CURRENT APPLICATION NUMBER: US/10/020,786

CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: US 60/256,164

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 8

LENGTH: 237

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: anti-Tf light chain

JS-10-020-786-8

Query Match

Best Local Similarity 61.1%; Score 754; DB 9; Length 237;

Matches 141; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

QY

16 TGARCDIQMTOSPASLSASVGETVTITCRASGNIONYLAWYQOTGKSPQLLVYSAKTLA 75

Db

19 TNAYADIQMTOSPSSLSASVGDRTVTITCRASRDIKSYLNWYQKPGKAPKVLIIYATSLA 78

QY

76 DGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGGTKLEIKRADAAPTV 135

Db

79 EGVPSRFSGSGGTDTYLTITSSLOPEDFATYYCLOHGESPWTFGGKVEIKRTVAAPSV 138

QY

136 SIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTDDQSKDSTYSM 195

Db

139 FIFPPSDEQLKSGTASVVCVLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYSL 198

QY

196 SSTLTLDKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234

Db

199 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 15

JS-10-227-694-4

Sequence 4, Application US/10227694

Publication No. US20030077739A1

GENERAL INFORMATION:

APPLICANT: Simmons, Laura

APPLICANT: Andersen, Dana

TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY

FILE REFERENCE: P1867R1

CURRENT APPLICATION NUMBER: US/10/227,694

CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: US 60/315,209

PRIOR FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 4

LENGTH: 237

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-227-694-4

Query Match

Best Local Similarity 61.1%; Score 754; DB 9; Length 237;

Matches 141; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

OM protein - protein search, using sw model  
Run on: June 18, 2003, 16:42:37 ; Search time 11.5028 Seconds  
(without alignments)  
598.546 Million cell updates/sec

Title: US-09-770-916-4  
Perfect score: 1234  
Sequence: 1 MSVLTQVLLALLLWLTGARC.....EATHTSTSPVKSFRNEC 234

Scoring table: BLSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/6C.COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	97.2	234	5	PCT-US94-07659-4
2	1131	91.7	236	2	US-08-792-824-3
3	1131	91.7	236	2	US-08-792-824-9
4	1131	91.7	236	2	US-08-792-824-12
5	1080	87.5	233	2	US-08-792-824-6
6	955	77.4	234	2	US-07-690-192-2
7	930.5	75.4	239	1	US-08-353-400-37
8	924	74.9	215	2	US-08-737-129A-8
9	907.5	73.5	235	4	US-09-423-439-58
10	907.5	73.5	235	4	US-09-011-769A-23
11	907	73.5	211	4	US-09-170-769A-8
12	901	73.0	218	5	PCT-US94-14106-57
13	888.5	72.0	219	1	US-08-353-400-34
14	883.5	71.6	235	2	US-08-303-569B-5
15	883.5	71.6	235	2	US-08-116-247-5
16	881.5	71.4	238	3	US-09-192-545-4
17	868	70.3	213	2	US-08-737-129A-4
18	855.5	69.3	215	6	5455030-3
19	845	68.5	215	4	US-09-170-769A-4
20	818	66.3	218	5	PCT-US94-14106-61
21	792	64.2	236	1	US-08-157-101A-5
22	790	64.0	206	6	5189147-9
23	771	62.5	214	3	US-08-397-411-5
24	759	61.5	233	2	US-07-934-373C-25
25	759	61.5	233	3	US-08-437-642B-25
26	759	61.5	233	4	US-08-146-206C-25
27	759	61.5	233	5	PCT-US93-07832-25

Query Match

97.2% ; Score 1200; DB 5; Length 234;

28	756.5	61.3	232	1	US-08-704-744-80
29	751	60.9	237	3	US-09-097-309-6
30	751	60.9	237	4	US-09-097-171A-10
31	751	60.9	237	4	US-09-422-712B-2
32	751	60.9	237	4	US-09-607-756-2
33	751	60.9	237	4	US-09-460-587-6
34	748	60.6	235	3	US-08-812-586-16
35	745	60.4	214	2	US-07-934-373C-39
36	745	60.4	214	3	US-08-437-642B-39
37	745	60.4	214	3	PCT-US93-07832-39
38	744	60.3	214	2	US-07-934-373C-40
39	744	60.3	214	2	US-08-788-800-11
40	744	60.3	214	3	US-08-437-642B-40
41	744	60.3	214	3	US-09-097-309-2
42	744	60.3	214	4	US-09-097-171A-2
43	744	60.3	214	4	US-09-460-587-2
44	744	60.3	214	5	PCT-US93-07832-40
45	743	60.2	237	2	US-08-463-587A-25

## ALIGNMENTS

RESULT 1  
PCT-US94-07659-4  
; Sequence 4, Application PC/TUS9407659  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurie, Mark  
; APPLICANT: Jackson, Jeffrey R.  
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
; NUMBER OF INVENTIONS: Disorders in Man  
; CORRESPONDENCE ADDRESS: 21  
; ADDRESSEE: SmithKline Beecham Corporation - Corp.  
; ADDRESSEE: Intellectual Property  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
FAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-07659-4

Sequence 80, Appl  
Sequence 6, Appl  
Sequence 10, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 6, Appl  
Sequence 16, Appl  
Sequence 39, Appl  
Sequence 39, Appl  
Sequence 39, Appl  
Sequence 40, Appl  
Sequence 11, Appl  
Sequence 40, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 40, Appl  
Sequence 25, Appl

us-09-770-916-4.ra

ue Jul 1 18:41:06 2003

Best Local Similarity 97.0%; Pred. No. 5.3e-90; Indels 0; Gaps 0;  
Matches 227; Conservative

1 MSVLTQVALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNITONYLAWYQOTQ 60  
1 MSVLTQVALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNITONYLAWYQOTQ 60  
61 GKSPQLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 120  
61 GKSPQLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 120  
121 GTKLEIKRADAAPTVSIFFPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVL 180  
121 GTKLEINRADAAPTVSIFFPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVL 180  
181 NSWTDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREC 234  
181 NSWTDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 2

US-08-792-824-3  
Sequence 3, Application US/08792824  
Patent No. 5932449  
GENERAL INFORMATION:  
APPLICANT: EMANUEL, PETER A.  
APPLICANT: BURANS, JAMES P.  
APPLICANT: VALDES, JAMES J.  
APPLICANT: MOHVEE, ELDEFRAWI E.  
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: U.S. Army Chemical and Biological Defense  
STREET: Office of the Chief Counsel, Bldg E4435  
CITY: Aberdeen Proving Ground  
STATE: MD  
COUNTRY: U.S.  
ZIP: 21010-5423  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,824  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Biffoni, U. J.  
REGISTRATION NUMBER: 39,908  
REFERENCE/DOCKET NUMBER: DAM 431-96  
TELEPHONE: 410-671-1158  
TELEFAX: 410-671-2534  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-792-824-3

Query Match 91.7%; Score 1131; DB 2; Length 236;

Best Local Similarity 93.9%; Pred. No. 2.1e-84; Indels 0; Gaps 0;

Matches 216; Conservative

5 TQVLAALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNITONYLAWYQOTQ 64

7 TAAAGLLLLAAQPMADIQMTQSPASLSASVGETVITCRASGNITONYLAWYQOTQ 66

65 QLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 120

67 QLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 126

125 EIKRADAAPTYSIIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWT 184

127 EIKRADAAPTYSIIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWT 186

185 DQSDKSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREC 234

187 DQSDKSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREC 236

US-08-792-824-9

Query Match 91.7%; Score 1131; DB 2; Length 236;

Best Local Similarity 93.9%; Pred. No. 2.1e-84; Indels 0; Gaps 0;

Matches 216; Conservative

5 TQVLAALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNITONYLAWYQOTQ 64

7 TAAAGLLLLAAQPMADIQMTQSPASLSASVGETVITCRASGNITONYLAWYQOTQ 66

65 QLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 120

67 QLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 126

125 EIKRADAAPTYSIIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWT 184

67 QLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 126

125 EIKRADAAPTYSIIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWT 184

127 EIKRADAAPTYSIIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWT 186

185 DQSDKSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREC 234

187 DQSDKSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREC 236

US-08-792-824-9

Sequence 3, Application US/08792824

Patent No. 5932449

GENERAL INFORMATION:

APPLICANT: EMANUEL, PETER A.

APPLICANT: BURANS, JAMES P.

APPLICANT: VALDES, JAMES J.

APPLICANT: MOHVEE, ELDEFRAWI E.

TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: U.S. Army Chemical and Biological Defense

STREET: Office of the Chief Counsel, Bldg E4435

CITY: Aberdeen Proving Ground

STATE: MD

COUNTRY: U.S.

ZIP: 21010-5423

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/792,824

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Biffoni, U. J.

REGISTRATION NUMBER: 39,908

REFERENCE/DOCKET NUMBER: DAM 431-96

TELEPHONE: 410-671-1158

TELEFAX: 410-671-2534

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 236 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-792-824-9

Query Match 91.7%; Score 1131; DB 2; Length 236;



ZIP: 08543-4000  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/07/690,192  
 APPLICATION NUMBER: 19910422  
 FILING DATE: 19910422  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bogden, James M  
 REGISTRATION NUMBER: 32,962  
 REFERENCE/DOCKET NUMBER: DC13  
 TELEPHONE: (609) 921-4163  
 TELEFAX: (609) 921-4526  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 234 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IS-07-690-192-2

Query Match 77.4%; Score 955; DB 2; Length 234;  
 Best Local Similarity 76.9%; Pred. No. 3.7e-70;  
 Matches 180; Conservative 25; Mismatches 29; Indels 0; Gaps 0;  
 1 MSVLTQVIALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60  
 1 MAIPTQLGLLLWLTDAICDIQMTQSPHLSLSIGETVSTECLEASGINSYLAWYQOKP 60  
 61 GKSPQLIYVSAKTLADGVPSRFGSGGTQYSLKINSIQPEDFGSYCQHFWSPTYFGG 120  
 61 GKSPQLIYVSAKTLADGVPSRFGSGGTQYSLKINSIQPEDFGSYCQHFWSPTYFGG 120  
 121 GTKLEIKRADAAPTVSIPTSPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRONGVL 180  
 121 GTKLEIKRADAAPTVSIPTSPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRONGVL 180  
 181 NSWTDQDSKDYSTMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234  
 181 DSVTDQDSKDYSTMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234

RESULT 7  
 US-08-353-400-37  
 ; Sequence 37, Application US/08353400  
 ; Patent No. 5665357  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: PROTEINS  
 ; NUMBER OF SEQUENCES: 37  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/353,400  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9324819.3  
 ; FILING DATE: 03-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9411089.7  
 ; FILING DATE: 03-JUN-1994  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 239 amino acids  
 ; TYPE: amino acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-353-400-37  
 Query Match 75.4%; Score 930.5; DB 1; Length 239;  
 Best Local Similarity 75.0%; Pred. No. 3.6e-68;  
 Matches 180; Conservative 22; Mismatches 31; Indels 7; Gaps 2;  
 1 MSVLTQVIALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 54  
 1 MDSQAQVLIILLWVSGTGDVMSQSPSLAVSAGEKVTMSCKSSQSLNLSRTRKNYLA 60  
 55 WYQOTQCKSPQLIYVSAKTLADGVPSRFGSGGTQYSLKINSIQPEDFGSYCQHFWSPT 114  
 61 WYQORPGOSPKLLIYWASTRFTSGVDPDRFTSGSGSTDTFLTISSVQAEADLAIYCKQSY-T 119  
 115 PYTFGGTGLEIKRADAAPTVSIPTSPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSE 174  
 120 LRTEGGTGLEIKRADAAPTVSIPTSPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSE 179  
 175 RQGVLSNWTDDQDSKDYSTMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234  
 180 RQGVLSNWTDDQDSKDYSTMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 239

RESULT 8  
 US-08-737-129A-8  
 ; Sequence 8, Application US/08737129A  
 ; Patent No. 5885816  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ikuo FUJII et al.  
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY  
 ; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Wenderoth, Lind & Ponack  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/737,129A  
 ; FILING DATE: No. 5885816ember 15, 1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33,367  
 ; REFERENCE/DOCKET NUMBER:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-8850  
 ; TELEFAX:  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 215 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-737-129A-8  
 Query Match 74.9%; Score 924; DB 2; Length 215;  
 Best Local Similarity 81.3%; Pred. No. 1.1e-67;



Matches	174;	Conservative	15;	Mismatches	25;	Indels	0;	Gaps	0;
QY	21	DIQMTQSPASLSASVGETVTITCRASGNITQNYLAWVQQTQKSPQLLVYSAKTLADGVPS	80						
Db	1	ELVMTQTPSSMYASLGRVTITCKASQDINILYLSWFWQKPGKSPKALIVRTINGLVGVPS	60						
QY	81	RFSGSGSGYQSLIKINSLOPEFGSYCYCOHFWSTPYTFGGGTGKLEIKRADAAPTVSIFPP	140						
Db	61	RFSGSGSGDYSLTISLSLEYEDMGIVCYQYDEFPYTFGGGTGKLEIKRADAAPTVSIFPP	120						
QY	141	SSEQLTSGGASVVCFLNNFPYPKDINVKWKIDGSEKQNGVLNSWTDQSDKSTYSMSSTLT	200						
Db	121	SSEQLTSGGASVVCFLNNFPYPKDINVKWKIDGSEKQNGVLNSWTDQSDKSTYSMSSTLT	180						
QY	201	LTKDSEYRHNSTYCEATHKTSTSPIVKGFNRNEC	234						
Db	181	LTKDSEYRHNSTYCEATHKTSTSPIVKGFNRNEC	214						

RESULT 9  
US-09-423-439-58  
; Sequence 58, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER: READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>

```

CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
S-09-423-439-58

```

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Query Match      73.5%; Score 907.5; DB 4; Length 235;  
Best Local Similarity 74.6%, Pred. No. 2.6e-66;  
Matches 176; Conservative 20; Mismatches 37; Indels 3; Gaps 2:  
  
1 MSVLTQVLALL--WLTGARDCTQMTQSASLSASVGCVTTTCRASGNIQNYLAWYQQ 58  
| | | : | | : | : | : | | | | | | | | | | : | | |  
1 MDFQVQIFSLILSASVINGRGQVLVSQPAILLASPGKVTMTCRASSSV-TVIHWYQQ 59  
| | | : | | | | | | | | | | | | | | | : | | |  
  
59 TQKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPDFGSYCQHFWSTPYTF 118  
| | | : | | | | | | | | | | | | | | | : | | |  
60 KPGSSPKSWIAYNSLASGVPARFSGSGSGTSYLTSIRVEADAATYYCQHWSSKPPTF 119  
| | | | | | | | | | | | | | | | | | | | | | | |  
119 GGGTKLEIKRAADAAPTYSIFPPSQEQLTSGGASVCFLNNFYPKDINVKKIDGSRQNG 178  
| | | | | | | | | | | | | | | | | | | | | | | |  
120 GGGTKLEIKRAADAAPTYSIFPPSQEQLTSGGASVCFLNNFYPKDINVKKIDGSRQNG 179
```

QY	179	VLSNWTQDQSKDSTYSMSSTLT	TKDEYRHNSYTCEATHKTSTSPIVKSFRN	EC 234
Db	180	VLSNWTQDQSKDSTYSMSSTLT	TKDEYRHNSYTCEATHKTSTSPIVKSFRN	EC 235

RESULT 10

US-09-011-769A-23

; Sequence 23, Application US/09011769A

; Patent No. 6436691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; BLAKEY, David C.

; DAVIES, David H.

; HENNAM, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998

PRIOR CLASSIFICATION: <Unknown>  
 APPLICATION NUMBER: PCT/GB96/01975  
 FILING DATE: 13-AUG-1996  
 APPLICATION NUMBER: GB 9612295.7  
 FILING DATE: 12-JUN-1996  
 APPLICATION NUMBER: GB 9611019.2  
 FILING DATE: 25-MAY-1996  
 APPLICATION NUMBER: GB 9516810.0  
 FILING DATE: 16-AUG-1995  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 235 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
 3'-091-011-769A-23

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Query Match      73.5%; Score 907 5; DB 4; Length 235;
Best Local Similarity 74.6%; Pred. No. 2.6e-66;
Matches 176; Conservative 20; Mismatches 37; Indels 3; Gaps 2;

      1 MSVLTVQLALLL--WLTGARCDTQMTQSPASIASASGETVTTTCRASGNIQNLAWYQQ 58
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      1 MDFQVQIFSFLLISASVIMSRGQTVLSQSFAILIASPCEKVTTCRASSV--TYIIHWYQ 59

59  TQCKSPOLLVYSAKTTLADGVSPRFSGSGSTQYSLKINSLQPDGFGSYGCOHFWSTPYTF 118
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      60 KPGSSPKSWIYATSNLASGVPAERFSGSGCTSYSLISRVEADAATYYICOHWSSKPTTF 119

119  GGCTKLEIKRADAAPTIVSPPPSSQLTSGGASVWCFLNNFYPKDINVKWKIDGSRQNG 178
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
120  GGCTKLEIKRADAAPTIVSIFPPSSQLTSGGASVWCFLNNFYPKDINVKWKIDGSRQNG 179

179  VLNSWTDQDSKDYTSMSSTLTLTKDYEYRHNSYTCETHKSTSPISVKSFNNEC 234
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
180  VLNSWTDQDSKDYTSMSSTLTLTKDYEYRHNSYTCETHKSTSPISVKSFNNEC 235
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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17. Mismatches	28. Indels	4: Gaps	1:
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[illegible]

## RESULT 13

```

US-08-353-400-34
Sequence 34, Application US/08353400
Patent No. 565357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA: US/08/353,400
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-34

```

Query Match	72.0%;	Score 888.5;	DB 1;	Length 219;
Best Local Similarity	77.3%;	Pred. No. 8.2e-65;		
Matches 170; Conservative	20;	Mismatches 23;	Indels 7;	Gaps 2;

21	DIQWTSQ	PASLSASV	GETVIT	ICRASGNI	-----QNYLAWQQQPGKSPOLLYISAKIL	74
	1	DIVMSQSP	SLAVSAGEK	VTMSCK	SSQSLLNSRTRKNLYAWQQRPGQSPKLLIYWASTR	60
	75	ADGVPSR	FGSGSGTQ	YSIKINSLO	PEDFGSYYCQHFWSPTVTFGGGTYKLEIKRADAAPT	134
	61	TSQVPDR	FTGSGSDT	FTLTIS	SSQAEDLAIYYCQSY-TLFTFGGGTYKLEIKRADAAPT	119
	135	VSIFPPS	SEQLTSGG	ASVCFLN	FPKDIINVKWKIDGSEKRGVNLNSWTDQDSKDSYSTS	194
	120	VSIFPPS	SEQLTSGG	ASVCFLN	FPKDIINVKWKIDGSEKRGVNLNSWTDQDSKDSYSTS	179
	195	MSSTLT	LTKDEYER	HNYSYTC	EATHKTSSTPIVKSFNRNEC	234
	180	MSSTLT	LTKDEYER	HNYSYTC	EATHKTSSTPIVKSFNRNEC	219

## RESULT 14

Query Match	73.08;	Score 901;	DB 5;	Length 218;
Best Local Similarity	77.58;	Pred. No. 7.9e-66;		

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:53 ; Search time 32.2079 Seconds  
(without alignments)  
968.107 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLQVLALLLLWLTGARC.....EATHKTSTSPVKSFRNREC 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
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- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	97.2	234	16 AAW11918	Murine MAB SK48-E2
2	1131	91.7	236	20 AAY30116	Murine anti-botuli
3	1131	91.7	236	20 AAY30120	Murine anti-botuli
4	1131	91.7	236	20 AAY30122	Murine anti-botuli
5	1080	87.5	233	20 AAY30118	Murine anti-botuli
6	955	77.4	234	20 AAY14557	Anti-p21(ras) mono
7	947	76.7	214	18 AAW27089	Mouse monoclonal a
8	930.5	75.4	239	16 AAW76087	MAB 55.1 light cha
9	925	75.0	238	23 AAE18371	Human penton base
10	924	74.9	216	17 AAW15935	Antibody 3G2 light

11	918	74.4	238	19 AAW83042	Anti-Fas MAB HFE7A
12	918	74.4	238	21 AAB14748	Mouse anti-Fas ant
13	918	74.4	238	21 AAW90898	Murine anti-Fas an
14	918	74.4	238	23 ABB74867	Humanised anti-Fas
15	918	74.4	238	23 ABB74913	Humanised anti-Fas
16	909.5	73.7	235	15 AAR47449	T84.12 light chain
17	909.5	73.7	235	15 AAR47451	T84.12 L4-12-1 lig
18	909	73.7	220	15 AAR53802	FAB light chain fo
19	907.5	73.5	235	17 AAW06178	Murine A5B57 Light
20	907.5	73.5	235	20 AAW82746	Plasmid pEE14/A5B7
21	904.5	73.3	215	15 AAR53803	FAB light chain fo
22	902	73.1	223	5 AAP40031	Kappa anti-carcino
23	901.5	73.1	215	14 AAR43674	Mouse anti-bovine
24	901	73.0	218	16 AAR75457	Mouse antibody FB3
25	901	73.0	218	16 AAR75459	Mouse antibody F4-
26	897	72.7	222	18 AAW01751	MH1 monoclonal ant
27	896.5	72.6	215	17 AAR99644	Anti-bGH monoclonal
28	895.5	72.6	215	17 AAR97377	Murine anti-BGH MA
29	892	72.3	214	23 ABB76125	Recombinant 4G10 a
30	888.5	72.0	219	16 AAR76086	MAB 55.1 light cha
31	888	72.0	214	21 AAW78253	Mouse agglutinin
32	885.5	71.8	239	16 AAR68757	Anti-tobacco mosai
33	884.5	71.7	213	10 AAP93035	Chimeric antibody
34	884.5	71.7	238	18 AAW31752	L chain subunit of
35	884.5	71.7	238	19 AAW71889	Anti-human Fas mon
36	884.5	71.7	238	21 AAB12909	Anti-human Fas ant
37	883.5	71.6	235	12 AAR13060	Monoclonal antibod
38	881.5	71.4	238	20 AAY17416	Mouse immunoglobul
39	881	71.4	236	13 AAR22565	Vilys-HuKappa reg
40	878.5	71.2	573	22 AAG64459	Mouse 6D9 catalyti
41	875.5	70.9	213	22 AAW50205	Type II collagen f
42	874.5	70.9	219	21 AAY95258	WOW-1 Fab light ch
43	874.5	70.9	234	23 AAW72802	TRA-8 light chain.
44	873	70.7	209	16 AAR64204	Monoclonal antibod
45	870.5	70.5	219	14 AAR44495	Sequence of the im

#### ALIGNMENTS

#### RESULT 1

AAW11918  
ID, AAW11918 standard; Protein; 234 AA.

XX AAW11918;

DT '24-JUN-1997 (first entry)

DE Murine MAB SK48-E26 light chain.

Interleukin-1 beta; IL-1 beta; recombinant antibody;  
humanised antibody; chimeric antibody; antibody engineering;  
monoclonal antibody; MAB; SK48-E26; inflammation; therapy.

OS Homo sapiens.

XX Key

FT Peptide

FT Location/Qualifiers

FT 1..20

FT /label= Sig\_peptide

FT 21..43

FT /label= FR1

FT /note= "framework region 1"

FT 44..54

FT /label= CDRI

FT /note= "complementarity determining region 1

FT (Claim 10, page 48)"

FT 55..69

FT /label= FR2

FT /note= "framework region 2"

FT 70..76

FT /label= CDR2

FT /note= "complementarity determining region 2

FT (Claim 10, page 48)"

Region 77..108  
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/note= "framework region 3"  
109..117  
/label= CDR3  
/note= "complementarity determining region 3  
(Claim 10, page 48)"  
Region 118..127  
/label= FR4  
/note= "framework region 4"  
128..234  
/label= Constant\_region  
W09501997-A1.  
19-JAN-1995.  
07-JUL-1994; 94WO-US07659.  
09-JUL-1993; 93US-0090534.  
04-MAR-1994; 94US-0206190.  
(SMIK ) SMITHKLINE BEECHAM CORP.  
Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;  
Young PR;  
WPI: 1995-066868/09.  
N-PSDB; AAT51437.  
Recombinant and humanised chimeric antibodies against human  
interleukin-1-beta - for preventing and treating  
interleukin-mediated inflammatory disorders  
Claim 5; Page 38-39; 62pp; English.  
Amino acid sequences of the heavy chain (AAW11917) and light chain  
(AAW11918) of anti-human interleukin-1 beta (IL-1 beta) murine  
monoclonal antibody (Mab) SK48-E26 were deduced from nucleic acids  
(AAT51436-37) derived from hybridoma SK48-E26. The heavy and light  
chains, esp. the complementarity determining region sequences,  
can be utilised in novel recombinant chimeric and humanised  
antibodies (see also AAW11919-20) useful for the treatment and  
prevention of IL-1 mediated inflammatory disorders.

Query Match 97.2%; Score 1200; DB 16; Length 234;  
Best Local Similarity 97.0%; Pred. No. 9.4e-69;  
Matches 227; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MSVLTQVIALLLWLTGACDIQMTQSPASLSASVGETVITTCRAGNIGNYLAWYQQTQ 60  
1 MSVLTQVIALLLWLTGACDIQMTQSPASLSASVGETVITTCRAGNIGNYLAWYQQTQ 60  
Db  
QY 61 GKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTFTGG 120  
61 GKSPOLLVYNAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTFTGG 120  
Db  
QY 121 GPKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGYL 180  
121 GPKLEINRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGYL 180  
Db  
QY 181 NSWTDQDSDSYMSSTLTTLTKDEYERHNSYTCBATHKTSTSPIVKSFNRNEC 234  
181 NSWTDQDSDSYMSSTLTTLTKDEYERHNSYTCBATHKTSTSPIVKSFNRNEC 234  
Db

RESULT 2  
AAY30116  
ID AAY30116 standard; Protein; 236 AA.  
XX  
AC AAY30116;

XX 20-OCT-1999 (first entry)  
DT Murine anti-botulinum toxin antibody fragment (BotFab 5) light chain.  
DE Recombinant antibody fragment; rFab; botulinum; neurotoxin;  
XX Clostridium botulinum; detection.  
KW Mus musculus.  
XX US5932449-A.  
PN 03-AUG-1999.  
PD 30-JAN-1997; 97US-0792824.  
XX 01-FEB-1996; 96US-0011013.  
PR 30-JAN-1997; 97US-0792824.  
XX (USSA ) US SEC OF ARMY.  
XX Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;  
PI WPI: 1999-492692/41.  
DR N-PSDB; AAX86664.  
XX Detection of botulinum toxin  
PT Claim 1; Columns 17-20; 24pp; English.  
PS This sequence represents the light chain of BotFab 5,  
CC a murine recombinant antibody fragment (rFab) specific to  
CC botulinum toxin types A and B. A cDNA library was made from mouse mRNA  
CC isolated from mice immunised with human pentavalent toxoid. The cloned  
CC mouse heavy and light chains were expressed in phage display libraries  
CC and screened for their ability to bind to botulinum toxin types A or B.  
CC The clones were then isolated and sequenced. Botulinum neurotoxin is  
CC produced as several antigenically distinct serotypes (A-G) and is  
CC non-covalently associated with non-neurotoxic proteins. The rFab of  
CC this invention binds to the non-neurotoxic proteins that are found in  
CC neurotoxin complexes A and B. Such antibody fragments are able to  
CC act as immunosensors for detecting botulinum toxins in food and  
CC are also useful in health care and in military applications. They  
CC are less expensive to produce than monoclonal antibodies as they can be  
CC isolated from large scale bacterial cultures. Also, the affinity of an  
CC rFab may be altered by mutagenesis of its gene and subsequent screening  
CC of the expressed rFabs.

Query Match 91.7%; Score 1131; DB 20; Length 236;  
Best Local Similarity 93.9%; Pred. No. 2.2e-64;  
Matches 216; Conservative 2; Mismatches 12; Indels 0; Gaps 0;  
QY 5 TOVLALLLWLTGACDIQMTQSPASLSASVGETVITTCRAGNIGNYLAWYQQTQKSP 64  
Db 7 TAAAGLLLLAAQAPAMADIQMTQSPASLSASVGETVITTCRAGNIGNYLAWYQQTQKSP 66  
QY 65 QLVVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTFTFGGKTL 124  
Db 67 QLVVYNAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTFTFGGKTL 126  
QY 125 ELKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWT 184  
Db 127 ELKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWT 186  
QY 185 DQDSDSYMSSTLTTLTKDEYERHNSYTCBATHKTSTSPIVKSFNRNEC 234  
Db 187 DQDSDSYMSSTLTTLTKDEYERHNSYTCBATHKTSTSPIVKSFNRNEC 236

RESULT 3  
AAY30120



```

|||||
187 DQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSPIVKSFRNEC 236
|||||
Db DB EIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVLSWT 186
QY 185 DQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSPIVKS 228
|||||
Db DB DQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSPIVKS 230
|||||
RESULT 6
AAY14557
ID AAY14557 standard; Protein; 234 AA.
XX
AC AAY14557;
XX
DT 31-AUG-1999 (first entry)
XX
DE Anti-p21(ras) monoclonal antibody Y13-259 light chain.
XX
KW Inhibition: function; recombinant; p21; ras; monoclonal antibody;
KW light chain; activity; cancer; neoplasm; oncogene.
XX
OS Mus sp.
XX
PN US5919650-A.
XX
PD 06-JUL-1999.
XX
PF 22-APR-1991; 91US-0690192.
XX
PR 22-APR-1991; 91US-0690192.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Barbacid M, Montano X;
XX
WPI; 1999-394621/33.
DR N-PSDB; AAX79347.
XX
Inhibiting protein function using recombinant, intracellularly
expressed antibodies
XX
Example 1; Column 15-16; 23pp; English.
XX
The invention relates to a method for inhibiting protein function using
recombinant, intracellularly expressed anti-protein antibodies (or
fragments). The protein function to be inhibited is preferably p21(ras).
It is especially inhibited by the monoclonal antibody Y13-259. This
sequence represents the light chain of the Y13-259 antibody. The method
may be used to inhibit the activity of specific proteins in cells and
eliminate undesirable biological responses, e.g. it may be used to treat
conditions associated with the over-expression or overactivity of the
target protein. In this way the method may be used to treat cancer and
neoplasms, by targeting proteins encoded by oncogenes.
XX
Sequence 234 AA:
Query Match 77.4%; Score 955; DB 20; Length 234;
Best Local Similarity 76.9%; Pred. No. 3e-53;
Matches 180; Conservative 25; Mismatches 29; Indels 0; Gaps 0;
QY 1 MSVLTQVLALLLWLTGARCIDIOMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 60
Db 1 MAIPTQLGLLLWLTDAICDIQMTQSPHLSASLGETVSIETCLASEGISNLYAWYQKP 60
QY 61 GKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSIQSLQDFGYSYCOHFWSPTPTFG 120
Db 61 GKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSIQSLQDFGYSYCOHFWSPTPTFG 120
QY 121 GTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVL 180
Db 121 GTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVL 180
QY 181 NSWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCATHKTSPIVKSFRNEC 234
|||||

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Db 181 DSVTDQDSKSTYSMSSTLSLTKEVEYERHNLTYTCEVVHKTSSSPVAKSFNRNEC 234

RESULT 7  
AAW27089  
ID AAW27089 standard; Protein; 214 AA.  
XX  
XX AAW27089;  
XX  
XX 18-NOV-1997 (first entry)  
XX  
XX Mouse monoclonal antibody B9 light chain.  
XX  
XX Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;  
XX  
XX antibody; Fab.  
XX  
XX Mus musculus.  
XX  
XX OS  
XX Key Location/Qualifiers  
XX Region 24..34  
XX FT /label= CDR1  
XX FT 50..56  
XX FT /label= CDR2  
XX FT 89..97  
XX FT /label= CDR3  
XX FT 108..214  
XX FT /label= Ckappa  
XX  
XX JP09154587-A.  
XX  
XX 17-JUN-1997.  
XX  
XX 09-MAY-1996; 96JP-0114492.  
XX  
XX 02-NOV-1995; 95KR-0039459.  
XX  
XX (KOAD ) KOREAN SCI & TECHNOLOGY RES CENT.  
XX  
XX WPI; 1997-367067/34.  
XX  
XX N-PSDB; AAT85091.  
XX  
XX DNA encoding mouse antibody binding human plasma apo-lipoprotein  
XX  
XX B-100 - useful for removing arteriosclerotic lipoprotein(s)  
XX  
XX Claim 4; Fig 6; 17pp; Japanese.  
XX  
XX The present sequence represents the mouse monoclonal antibody B9 light  
XX  
XX chain (B9L), which binds specifically to human blood apolipoprotein  
XX  
XX B-100. The nucleic acid can be used in a method for the preparation  
XX  
XX of a reconstituted antibody which specifically binds human plasma  
XX  
XX apolipoprotein B-100. The antibody can be used as a reagent for  
XX  
XX determining the concentration of human plasma apolipoprotein B-100  
XX  
XX in a sample. The antibody is also useful in a drug composition for  
XX  
XX selectively removing arteriosclerotic lipoproteins containing human  
XX  
XX plasma apolipoprotein B-100.  
XX  
XX Sequence 214 AA;  
XX  
XX Query Match 76.7%; Score 947; DB 18; Length 214;  
XX  
XX Best Local Similarity 83.6%; Pred. No. 8.9e-53;  
XX  
XX Matches 179; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 21 DIOMTQSPASLSASVGETVITCRASNTONYLAWYQOTGKSPQLLVYSAKTLADGVPS 80  
DB 1 DIKMTQSPSMYASLGERVITITCASQDIYVLSWFKQPKGPKTLIYRANRLVDGVPS 60

QY 81 RFSGSGSGTQYSLKINSLODPFGSYCOHFWSPTPTFGGKLETKRADAATVSIFPP 140  
DB 61 RFSGSGSGDYSLTISLSLEYEDLGIYCLQDFEFPYTFGGGKLETKRADAATVSIFPP 120

QY 141 SSEQLTSGASVYVCLNNFYPKDINVKWKIDGSEKQNGVLSNSTDODSKDSTYSMSSTLT 200  
DB 121 SSEQLTSGGASVYVCLNNFYPKDINVKWKIDGSEKQNGVLSNSTDODSKDSTYSMSSTLT 180

QY 201 LTKDEYERHNSYTCEATHKTTSTPIVKSFNRENC 234  
DB 181 LTKDEYERHNSYTCEATHKTTSTPIVKSFNRENC 214

RESULT 8  
AAR76087  
ID AAR76087 standard; Protein; 239 AA.  
XX  
XX AAR76087;  
XX  
XX 21-NOV-1995 (first entry)  
XX  
XX MAB 55.1 light chain.  
XX  
XX Antigen binding structure; complementarity determining region; CDR;  
XX  
XX CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
XX  
XX monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
XX  
XX transgenic animal; transgenic plant; antibody engineering;  
XX  
XX humanized antibody; immunotoxin.  
XX  
XX Mus sp.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..20  
XX FT /label= Sig\_peptide  
XX FT 21..239  
XX FT /label= Mat\_protein  
XX FT /note= "claim 3, page 98"  
XX  
XX WO9515382-A.  
XX  
XX 08-JUN-1995.  
XX  
XX 29-NOV-1994; 94WO-GB02610.  
XX  
XX 03-JUN-1994; 94GB-0011089.  
XX  
XX 03-DEC-1993; 93GB-0024819.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;  
XX  
XX Rose MS, Wright AF;  
XX  
XX WPI; 1995-215262/28.  
XX  
XX N-PSDB; AAQ94036.  
XX  
XX Antigen binding structures containing CDRs recognising the CA55.1  
XX  
XX antigen - produced by hybridomas and host cells, for use in the  
XX  
XX diagnosis and therapy of cancer  
XX  
XX Disclosure; Fig.16; 121pp; English.  
XX  
XX MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
XX  
XX antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
XX  
XX chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or  
XX  
XX V-min humanized 55.1 constructs have been expressed in myeloma  
XX  
XX cells and E. coli.  
XX  
XX Sequence 239 AA;

Query Match 75.4%; Score 930.5; DB 16; Length 239;  
Best Local Similarity 75.0%; Pred. No. 1.1e-51;  
Matches 180; Conservative 22; Mismatches 31; Indels 7; Gaps 2;

QY 1 MSVLTQVLAALLLWLTGARCIDIOMTQSPASLSASVGETVITCRASNI-----QNYLA 54  
DB 1 MDQQAQVLIILLWVSGTCGDIWMSQSPSLAVSAGEKVTMSCKSSQSLNRSRKNYLA 60

QY 55 WYQOTQCKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLODPFGSYCOHFWS 114  
DB 61 WYQORFGQSPKLLIYWASTRTSGVDPDRFTGGSGGTDTFLTITSSVQABDLAIYYCKQSY-T 119







Db 61 QOKPQPKLLIYAASNLESGIPARFSGSGTDFTLNHPVEEDAATYYCQOSNEDPR 120  
QY 117 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 176  
Db 121 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 180  
QY 177 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 234  
Db 181 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 238

RESULT 14  
ABB74867  
ID ABB74867 standard; Peptide; 238 AA.  
AC ABB74867;  
XX  
DT 26-APR-2002 (first entry)  
XX  
DE Humanised anti-Fas antibody related peptide SEQ ID NO 33.  
XX  
KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
KW autoimmune disease; allergy; atopic.  
XX  
OS Homo sapiens.  
XX  
PN JP2001342148-A.  
XX  
PD 11-DEC-2001.  
XX  
PF 28-MAR-2001; 2001JP-0093106.  
XX  
PR 29-MAR-2000; 2000JP-0090918.  
XX  
PA (SANY ) SANKYO CO LTD.  
XX  
DR WPI; 2002-145113/19.  
XX  
PT Drug containing humanised anti-Fas antibody, used for preventing and  
PT treating autoimmune diseases, allergy, and atopy -  
XX  
PS Example 6 (Preparatory); Page 26; 194pp; Japanese.  
XX  
CC The invention relates to a preventive or treating agent for diseases  
CC caused by abnormality in Fas/Fas ligand system containing as the active  
CC component an antibody having as the light chain subunit a polypeptide  
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
CC fully defined in the specification and having an activity of combining  
CC specifically with mammalian Fas and an activity of inducing apoptosis  
CC in a cell expressing Fas. The agent has immunosuppressive and  
CC antiallergic activity and is used for preventing and treating autoimmune  
CC diseases, allergy, atopy and others. The present sequence is that of a  
CC peptide, useful to the invention.  
SQ Sequence 238 AA;

Query Match 74.4%; Score 918; DB 23; Length 238;  
Best Local Similarity 72.3%; Pred. No. 6.7e-51;  
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

QY 1 MSVLTQVLAALLLWLTGARCIDIQTQSPASLASVGETVTITCRASGNI---QNYLAWY 56  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
1 METDTILLWVWMLTIPGSTGDIVLTQSPASLASVLCQRATISCKASQSDVDGDSYNNWY 60

Db 57 QOTQKSPOLLVYSAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYQCQHFWSPTY 116  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
61 QOKPQPKLLIYAASNLESGIPARFSGSGTDFTLNHPVEEDAATYYCQOSNEDPR 120

QY 117 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 176  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
121 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 180

QY 177 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 234  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
Db 181 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 238

36

Db 121 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 180  
QY 177 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 234  
Db 181 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 238

RESULT 15  
ABB74913  
ID ABB74913 standard; Peptide; 238 AA.  
AC ABB74913;  
XX  
DT 30-APR-2002 (first entry)  
XX  
DE Humanised anti-Fas antibody related peptide SEQ ID NO 3.  
XX  
KW Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;  
KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;  
KW autoimmune disease; allergy; atopy.  
XX  
OS Mus musculus.  
XX  
PN JP2001342149-A.  
XX  
PD 11-DEC-2001.  
XX  
PF 28-MAR-2001; 2001JP-0093243.  
XX  
PR 29-MAR-2000; 2000JP-0091144.  
XX  
PA (SANY ) SANKYO CO LTD.  
XX  
DR WPI; 2002-145114/19.  
XX  
PT Drug for preventing or treating e.g. autoimmune disease or allergy,  
PT comprises humanised anti-Fas antibody -  
XX  
PS Disclosure; Page 65; 154pp; Japanese.  
XX  
CC The invention relates to a preventive or treating agent for diseases  
CC caused by abnormality in the Fas/Fas ligand system containing, as the  
CC active component, an antibody having a light chain subunit and a heavy  
CC chain subunit and an activity of combining specifically with mammalian  
CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The  
CC agent has antiallergic, immunosuppressive and apoptotic activity and is  
CC used for preventing and treating autoimmune diseases, allergy, atopy and  
CC others. The present sequence is that of a peptide useful to the  
CC invention.

SQ Sequence 238 AA;

Query Match 74.4%; Score 918; DB 23; Length 238;  
Best Local Similarity 72.3%; Pred. No. 6.7e-51;  
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

QY 1 MSVLTQVLAALLLWLTGARCIDIQTQSPASLASVGETVTITCRASGNI---QNYLAWY 56  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
1 METDTILLWVWMLTIPGSTGDIVLTQSPASLASVLCQRATISCKASQSDVDGDSYNNWY 60

QY 57 QOTQKSPOLLVYSAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYQCQHFWSPTY 116  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
Db 61 QOKPQPKLLIYAASNLESGIPARFSGSGTDFTLNHPVEEDAATYYCQOSNEDPR 120

QY 117 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 176  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
Db 121 TFGGKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQ 180

QY 177 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 234  
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
Db 181 NGVLSWTDQDSKDYSSMSSTLTLTCKDEYERHNSYTCEATHKTSPIVKSFNNEC 238

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Search completed: June 18, 2003, 16:44:19  
Job time : 33.2079 secs

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